

BLASTN 2.2.19+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: URU2TF3R016

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

8,293,739 sequences; 26,430,693,440 total letters

Query= SID_3

Length=2660

Sequences producing significant alignments:	Score (Bits)	E Value
gb K00470.1 HUMGHV Homo sapiens growth hormone variant precur...	4913	0.0
gb J03071.1 HUMGHCSA Human growth hormone (GH-1 and GH-2) and...	4831	0.0
gb AC040958.20 Homo sapiens chromosome 17, clone RP11-630H24...	4806	0.0
gb EU421715.1 Homo sapiens growth hormone 2 precursor (GH2) ...	3949	0.0
gb AC127029.12 Homo sapiens chromosome 17, clone CTC-264K15,...	3864	0.0
gb M13438.1 HUMGHN Human growth hormone gene (HGH-N), complet...	3795	0.0
gb AC198149.2 Nomascus leucogenys BAC clone CH271-32K4 from ...	3413	0.0
emb CT954302.6 N.leucogenys DNA sequence from clone CH271-26...	3402	0.0
gb EU421712.1 Homo sapiens growth hormone 1 (GH1) gene, comp...	3254	0.0
gb AF374233.1 Pan troglodytes growth hormone (GH-V) gene, co...	3236	0.0
gb DQ002799.1 Macaca mulatta growth hormone 1 (GH-1), chorio...	3179	0.0
gb AC203687.3 MACACA MULATTA BAC clone CH250-171J17 from chr...	3072	0.0
gb AC015651.18 AC015651 Homo sapiens chromosome 17, clone RP1...	2957	0.0
gb K02401.1 HUMCS1 Human chorionic somatomammotropin gene hCS...	2950	0.0
gb M15895.1 HUMCS5 Human chorionic somatomammotropin CS-5 pse...	2929	0.0
gb J00289.1 HUMPLA Homo sapiens placental lactogen hormone pr...	2909	0.0
gb M15894.1 HUMCS3 Human chorionic somatomammotropin hCS-3 gene	2852	0.0
gb EU421714.1 Homo sapiens chorionic somatomammotropin hormo...	2811	0.0
gb EU421716.1 Homo sapiens chorionic somatomammotropin hormo...	2787	0.0
emb V00520.1 Human germ line gene for growth hormone (presom...	2784	0.0
gb EU421713.1 Homo sapiens chorionic somatomammotropin hormo...	2767	0.0
gb AF374232.1 Pan troglodytes growth hormone (GH-N) gene, co...	2741	0.0
gb AY146625.1 Pan troglodytes placental lactogen PL-A gene, ...	2689	0.0
gb AY146626.1 Pan troglodytes placental lactogen PL-B gene, ...	2507	0.0
gb DQ002803.1 Macaca mulatta chorionic somatomammotropin hor...	2440	0.0
gb AY146628.1 Pan troglodytes placental lactogen PL-D gene, ...	2411	0.0
gb U02293.1 MMU02293 Macaca mulatta growth hormone-variant ge...	2331	0.0
emb AM235212.1 Callithrix jacchus gh (growth hormone) gene r...	2272	0.0
gb AY146627.1 Pan troglodytes placental lactogen PL-C gene, ...	2263	0.0
emb AM235213.1 Cebus albifrons gh gene for growth hormone pr...	2233	0.0
emb AM260481.1 Cebus albifrons growth hormone like pseudogene 6	2226	0.0
gb AF285183.1 AF285183 Cloning vector pSGHV0, complete sequence	2217	0.0
gb AY621641.1 Nomascus leucogenys growth hormone-like protei...	2198	0.0
emb CR610932.1 full-length cDNA clone CS0DI030YP11 of Placen...	2170	0.0
emb CR595678.1 full-length cDNA clone CS0DI030YK15 of Placen...	2165	0.0
emb AM260482.1 Cebus albifrons growth hormone like pseudogene 7	2141	0.0
emb CR614095.1 full-length cDNA clone CS0DI083YB03 of Placen...	2130	0.0
gb AY621637.1 Nomascus leucogenys growth hormone-like protei...	2119	0.0
emb CR601644.1 full-length cDNA clone CS0DI053YA22 of Placen...	2111	0.0
gb AY621636.1 Nomascus leucogenys growth hormone-like protei...	2108	0.0
emb AM260483.1 Cebus albifrons growth hormone like pseudogene 8	2098	0.0

gb AY744456.1	Callicebus moloch growth hormone-like protein ...	2084	0.0
emb CR607774.1	full-length cDNA clone CS0DI076YA16 of Placen...	2045	0.0
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gb AY744453.1	Alouatta seniculus growth hormone-like protein...	2015	0.0
gb AY744459.1	Callicebus moloch growth hormone-like protein ...	2012	0.0
gb AY621647.1	Pygathrix roxellana growth hormone-like protei...	2002	0.0
gb AY744458.1	Callicebus moloch growth hormone-like protein ...	1980	0.0
gb AY621645.1	Pygathrix nemaeus growth hormone-like protein ...	1978	0.0
emb AJ489811.1	CJA489811 Callithrix jacchus ghlp6 gene for gr...	1978	0.0
gb AY621643.1	Pygathrix nemaeus growth hormone-like protein ...	1975	0.0
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gb DQ002802.1	Macaca mulatta chorionic somatommatotropin hor...	1925	0.0
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gb AY744464.1	Pithecia pithecia growth hormone-like protein ...	1881	0.0
gb AY744462.1	Pithecia pithecia growth hormone-like protein ...	1877	0.0
gb AF374235.1	Ateles geoffroyi growth hormone (GH-V) gene, c...	1855	0.0
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emb AJ489812.1	CJA489812 Callithrix jacchus ghlp7 pseudogene	1845	0.0
gb AY744463.1	Pithecia pithecia growth hormone-like protein ...	1845	0.0
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gb AY744454.1	Alouatta seniculus growth hormone-like protein...	1821	0.0
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gb AY621640.1	Nomascus leucogenys growth hormone-like protei...	1770	0.0
gb AY621635.1	Hylobates leucogenys growth hormone-like 1 (gh...	1770	0.0
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gb AY621651.1	Macaca assamensis growth hormone-like protein ...	1674	0.0
gb AY621652.1	Macaca assamensis growth hormone-like protein ...	1663	0.0
gb AY621648.1	Pygathrix roxellana growth hormone-like protei...	1657	0.0
emb AJ489810.1	CJA489810 Callithrix jacchus ghlp5 gene for gr...	1657	0.0
gb AY621646.1	Pygathrix nemaeus growth hormone-like protein ...	1653	0.0
gb AY621642.1	Pygathrix nemaeus growth hormone-like protein ...	1653	0.0
gb AY744455.1	Alouatta seniculus growth hormone-like protein...	1640	0.0
gb AY621654.1	Macaca assamensis growth hormone-like protein ...	1622	0.0
gb AY621650.1	Pygathrix roxellana growth hormone-like protei...	1611	0.0
gb AY621655.1	Macaca assamensis growth hormone-like protein ...	1581	0.0
gb AY435434.1	Ateles geoffroyi GH-C gene, partial cds	1541	0.0
ref NM_022557.2	Homo sapiens growth hormone 2 (GH2), transcr...	1319	0.0
gb J03756.1	HUMGHVA Human growth hormone-variant (GH1) and gr...	1308	0.0
emb CR621109.1	full-length cDNA clone CS0DI055YC07 of Placen...	1297	0.0
emb CR594288.1	full-length cDNA clone CS0DI039YO13 of Placen...	1221	0.0
ref XM_001156416.1	PREDICTED: Pan troglodytes similar to gro...	1127	0.0
ref XM_001156130.1	PREDICTED: Pan troglodytes similar to gro...	1105	0.0
emb CR603719.1	full-length cDNA clone CS0DI042YM19 of Placen...	1096	0.0
emb CR624740.1	full-length cDNA clone CS0DI069YK20 of Placen...	1051	0.0
emb CR592007.1	full-length cDNA clone CS0DI026YA17 of Placen...	1046	0.0
emb CR590740.1	full-length cDNA clone CS0DI024YB06 of Placen...	1046	0.0
ref NM_022640.2	Homo sapiens chorionic somatommatotropin hor...	1040	0.0
emb CR618773.1	full-length cDNA clone CS0DI027YA22 of Placen...	1038	0.0
emb CR590972.1	full-length cDNA clone CS0DI009YJ04 of Placen...	1038	0.0
emb CR619097.1	full-length cDNA clone CS0DI049YD11 of Placen...	1037	0.0
emb CR612411.1	full-length cDNA clone CS0DI081YA23 of Placen...	1031	0.0

Query	781	GAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCCTCCGGTTTCTCCCCAGGCTC	840
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Sbjct	841	CCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGGGCAG	900
Query	901	TGCCTTCCCAACCATTCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCGCCCGTCG	960
Sbjct	901	TGCCTTCCCAACCATTCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCGCCCGTCG	960
Query	961	CCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTAATGGGTGC	1020
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Query	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCGCTGGGAAGTAATGGGAGGAGACTA	1080
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Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCAATCCTGGGGCCCCAC	1620
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Query	2521	TAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCCC	2580
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Query   2581  AGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTGGGTCCACTC  2640
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Query   2641  AGTAGATGCTTGTTGAATTC  2660
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Sbjct   2641  AGTAGATGCTTGTTGAATTC  2660

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>gb|J03071.1|HUMGHCSA Human growth hormone (GH-1 and GH-2) and chorionic somatomammo (CS-1, CS-2 and CS-5) genes, complete cds
Length=66495

Score = 4831 bits (2616), Expect = 0.0
Identities = 2652/2667 (99%), Gaps = 12/2667 (0%)
Strand=Plus/Plus

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Query    61      TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG  120
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Sbjct   41648  TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG  41707

Query   121      GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA  180
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Sbjct   41708  GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA  41766

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Sbjct   41886  CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG  41945

Query   361      GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG  420
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Query   421      CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCAGGTATAAAAAGGGCCAC  480
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Sbjct   42006  CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCAGGTATAAAAAGGGCCAC  42065

Query   481      AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC  540
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Sbjct   42066  AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC  42125

Query   541      AGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTT-GGCACAATGT  598
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Sbjct   42126  AGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTTGGGCACAATGT  42185

Query   599      GTCCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG  658
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Sbjct	43085	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAG	43144
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Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTAGCAGTCAGGC	1675
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Sbjct	43265	GCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCTTTC	43324
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Sbjct	43565	AGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	43624
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Sbjct	43625	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTACTC	43684
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Query	2394	ACGGGGTTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC	2453


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Sbjct  43983  ACGGGGTTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCC  44042
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Sbjct  44043  GCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCCT  44102
Query  2514  GTGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGC  2573
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Sbjct  44103  GTGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGC  44162
Query  2574  CATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTGGG  2633
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Sbjct  44163  CATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTGGG  44222
Query  2634  TCCACTCAGTAGATGCTTGTGTAATTC  2660
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Sbjct  44223  TCCACTCAGTAGATGCTTGTGTAATTC  44249

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Score = 3886 bits (2104), Expect = 0.0
Identities = 2491/2675 (93%), Gaps = 38/2675 (1%)
Strand=Plus/Plus

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Query  1  GAATTCAGCACTGAATCATGCCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCT  60
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Sbjct  4671  GAATTCAGGACTGAATCGTGCTCACAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCT  4729
Query  61  TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG  120
          |||
Sbjct  4730  TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG  4789
Query  121  GAATAGGATAGAGAGTGGGATGGGGTCGGTA-GGGGTCTCAAGGACTGGCCTATCCTGAC  179
          | |||
Sbjct  4790  GGATAGGATAGAGAATGGGATGTGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGAC  4848
Query  180  ATCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACC  239
          |||
Sbjct  4849  ATCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCGGCCAGAGGGCACCCACGTGACC  4908
Query  240  CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACA  299
          |||
Sbjct  4909  CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACACTCTGTGCACAACCCTCACA  4968
Query  300  ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT  359
          || |||
Sbjct  4969  ACACTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGGCATGATCCCAGCATGTGT  5028
Query  360  GGGAGGAGCTTCTAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCCAGGCCTAAACAT  419
          |||
Sbjct  5029  GGGAGGAGCTTCTAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCCATGCATAAATGT  5088
Query  420  GCAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCC  478
          || |||
Sbjct  5089  ACACAGAAACAGGTG-GGGGCAA-CAGTGGGAGAGAAGGGGCCAGGTATAAAAAGGGCCC  5146
Query  479  ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGG  538
          |||
Sbjct  5147  ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGG  5206
Query  539  ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCTAAATCCCTTT-GGCACAAT  596

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Sbjct	6092	 CGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGGAGTGTC	6151
Query	1494	TTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCG-CCACCTGAAGGA	1552
Sbjct	6152	 TTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTAT-GACCTCCTAAAGGA	6210
Query	1553	CCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA-GGAT--CCAATCC	1609
Sbjct	6211	 CCTAGAGGAAGGCATCCAAACGCTGATGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCC	6270
Query	1610	TGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGCTGCCCTCTTTTATGCA	1668
Sbjct	6271	 TGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGCTGCCCTCTTTTATGCA	6329
Query	1669	GTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAG	1728
Sbjct	6330	 GTCAGGCCCTGACCCAAGAGAACTCACCTTATTCTTCATTTCCCCTCGTGAATCCTCCAG	6389
Query	1729	GCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAAC	1788
Sbjct	6390	 GCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGAATGAATGAGAAAGGGAGGGAAC	6449
Query	1789	AGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGCTGGAAGATGGC	1848
Sbjct	6450	 AGTACCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGCTGGAAGATGGC	6509
Query	1849	AGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCAC	1908
Sbjct	6510	 AGCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACAC	6569
Query	1909	AACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	1968
Sbjct	6570	 AACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	6629
Query	1969	AAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC	2028
Sbjct	6630	 AAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC	6689
Query	2029	TAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGT	2088
Sbjct	6690	 TAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTT	6749
Query	2089	GCTACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGTTGAC	2148
Sbjct	6750	 GCCACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTGAC	6809
Query	2149	TAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGT	2208
Sbjct	6810	 TAGGTGTCCTTCTATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCAAG-T	6868
Query	2209	TGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACCAGGCTGGAGTGCAGTGG	2268
Sbjct	6869	 TGGGAAGACAACCTGTAGGGCCTGCGGGTCTATTTCGGGAACCAAGCTGGAGTGCAGTGG	6928
Query	2269	CAG--TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGT	2326
Sbjct	6929	 CACAATCTTGGCTCACTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGC	6988
Query	2327	CTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTT	2386

Sbjct	6989	CTCCCCGAGTTGTTGGGATTCCAGGCATGCATGACCAGGCTCAGCTAATTTTTGTTTTTTTT	7048
Query	2387	GGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAA	2446
Sbjct	7049	GGTAGAGACGGGGTTTCACCATATTGGCCAGGCTGGTCTCCAACCTCCTAATCTCAGGTGA	7108
Query	2447	TCCGCCCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCC	2506
Sbjct	7109	TCTACCCACCTTGGCCTCCCAAATTGCTGGGATTACAGGCGTGAACCACTGCTCCCTTCC	7168
Query	2507	CTGTCCTG-TGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGC	2565
Sbjct	7169	CTGTCCTTCTGATTTTAAAATAACTATACCAGCAGGAGGACGTCCAGACACAGCATAGGC	7228
Query	2566	TACCTGGCCATGCCAGCCAGTTGGACATTTGAGTTGTTGCTTGGCACTGTCCTCTCAT	2625
Sbjct	7229	TACCTG-CCATGCCCAACCGGTGGGACATTTGAGTTGCTTGGCACTGTCCTCTCAT	7287
Query	2626	GCATTGGGTCCACTCAGTAGATGCTTGTTGAATTC	2660
Sbjct	7288	GCGTTGGGTCCACTCAGTAGATGCCTGTTGAATTC	7322

Score = 2970 bits (1608), Expect = 0.0
Identities = 2071/2288 (90%), Gaps = 58/2288 (2%)
Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATCATGCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT 	60
Sbjct	26916	GAATTCAGGACTCAATGGTGTCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT	26974
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 	120
Sbjct	26975	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGGAGGAGGAAAG	27034
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 	180
Sbjct	27035	GAATAGGATAGAGAGTGGAAATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA	27093
Query	181	TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACGTGACCC 	240
Sbjct	27094	GCCTTCCCCGCGTTTCAGGTTGACCAACATGGCCTGCAGCCAGAGGGGCACCCACCTGACCC	27153
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTA-TCTCTGGCTGACATTCTGTGCACAACCCTCACA 	299
Sbjct	27154	TTAAAGAGAGGACAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGCACAATCCTTACA	27212
Query	300	ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT 	359
Sbjct	27213	ACACTGGTGATGGTGAGAAGGGAAAGACGACAAGCCAGGGGGCATGATCCCAGCATGTGT	27272
Query	360	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACAT 	419
Sbjct	27273	GGGAGGAGCTTCTAAATTATCCACTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	27332
Query	420	GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC 	478
Sbjct	27333	ACACAGAAACAGGTGGGGTCAAGCAGGGAGAGAGAACTGGCCAGGGTATAAAAAGGGCCC	27392

Query	1356	ATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTG	1415
Sbjct	28280	ATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTG	28339
Query	1416	CAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTG	1475
Sbjct	28340	CAGAATCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCGTG	28399
Query	1476	CAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTC	1535
Sbjct	28400	CGGTTCTCAGGAGTATGTTTCGCCAACACCTGGTGTATGACACCTCGGACAGCGATGAC	28459
Query	1536	TATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCA	1595
Sbjct	28460	TATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGCG	28519
Query	1596	CCAGGA-TC-C-AATCCTGGGGCCCCACTGGCTTCCAGGGACTGGGG-AGAGAAACACTG	1651
Sbjct	28520	CCAGGGGTACCAATCCTGGAACCCCACTGGCTTCGAGGG-CTGGGGGAGAGAAATACTG	28578
Query	1652	CTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCC	1711
Sbjct	28579	CTGCCCTCTTTTTAGCAGTAAGGCGCTGACCCAAGAGAACTCACCTTATTCTTCATTTCC	28638
Query	1712	CCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAA	1771
Sbjct	28639	CCTGGTGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGG-AGGGAGGAAAATGGATAAA	28697
Query	1772	TGAGAGAGGG-AGGGAACAGTGCCCAAGCGCTTGG-CCTCTCCTTCTCTTCCTTCACTTT	1829
Sbjct	28698	TGAGAGAGGGGAGGGAACAGTGCCCAAGCGCTTGGACCTCTCCTTCTCTTCCTTCACTTT	28757
Query	1830	GCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAA	1889
Sbjct	28758	GCAGAGGCTGGAAGACGGCAGCCGCGGACTGGGCAGATCCTCAAGCAGACCTACAGCAA	28817
Query	1890	GTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTG	1949
Sbjct	28818	GTTTGACACAAACTCGCACAAACATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTG	28877
Query	1950	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGT	2009
Sbjct	28878	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGCAGTGCCGCTCTGT	28937
Query	2010	GGAGGGCAGCTGTGGCTTCTAGCTGCCCAGGTGGCATCCCTGTGACCCCTCCCCAGTGCC	2069
Sbjct	28938	GGAGGGCAGCTGTGGCTTCTAGGTGCCCAGTAGCATCC-TGTGACCCCTCCCCAGTGCC	28996
Query	2070	TCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCAGCCTTGTCCTAATAAAATTAAG	2129
Sbjct	28997	TCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCACCAGCCTTGTCCTAATAAAATTAAG	29055
Query	2130	TTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA-GGCGGGTGG	2188
Sbjct	29056	TTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGGAAGGTGG-TGG	29114
Query	2189	TATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCTATTTCGGG	2247
Sbjct	29115	TATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAAGGTCTATT-GGG	29170

Score = 2957 bits (1601), Expect = 0.0
Identities = 2072/2290 (90%), Gaps = 69/2290 (3%)
Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCTT 	60
Sbjct	12250	GAATTCAGGACTGAATCATGCTCACAACCCCAATCTATTGGCTGTGC-TTGGCCCTT	12308
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 	120
Sbjct	12309	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG	12368
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 	180
Sbjct	12369	GAATAGGATAGAGAGTGGGATGTGGTCGATAGGGGTCTCAAGGACTGG-CTATCCTGACA	12427
Query	181	TCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACGTGACCC 	240
Sbjct	12428	TCCTTCTCCGCATTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGGCACCCACCTGAACC	12487
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACAA 	300
Sbjct	12488	TTAAAGAGAGGACAAGTTGGGTGGTGTCTGTGGTTGACACTCTGTGCACAACCCTCACAA	12547
Query	301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG 	360
Sbjct	12548	CGCTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGACATGATGCCAGCATGTGTG	12607
Query	361	GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG 	420
Sbjct	12608	GGAGGAGCTTCCAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGTG	12667
Query	421	CAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC 	478
Sbjct	12668	CACAGAAACAGGTG-GGGGCAA-CAGCGAGAGAGAAGGGGCCAGGGTATAAAAAGGGCCC	12725
Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGG 	538
Sbjct	12726	ACAAGAGACCAGCTCCAGCATCCCAAGGCCCGACTCCCCGCACCACTCAGGGTCTGTGG	12785
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAAATCCCTTT-GGCACAAT 	596
Sbjct	12786	ACAGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAAATCCCTTTGGGCACAAC	12845
Query	597	GTGTCCTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTT 	656
Sbjct	12846	GTGTCCTGAGGGGAGAGGCGGCGCCCTGCAGATGGGACGGGGGCACTAA-CCTCAGGTTT	12904
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAG-TATTTGGCCAATCTCTGAATG 	715
Sbjct	12905	GGGGCTTCTGAATGTGA-ATATCGCCATCTAAGGCCAGATATTGGCCAATCTCTGAATG	12963
Query	716	TTCCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAAAAAAACCAGCTCCTGGA 	775
Sbjct	12964	TTCCTGGTCCCT---GGAGG--GA-TG-GAGAGAGAGAAAAAGAAAA--CAGCTCCTGGA	13014

Query	776	ACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCC 	834
Sbjct	13015	ACAGGGAGAGTGCTGGCCTCTTGCTCTGCGGCTCCCT-TCTTGCCCTCCGGTTTCTCCCC 	13073
Query	835	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCTCCTGGCTTCAAGA 	894
Sbjct	13074	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGA 	13133
Query	895	GGGC-AGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACA-ACGCTATGCTCCGC 	952
Sbjct	13134	-GGCTGGTGCCGTCCAAACCGTTCCTTATCCAGGCTTTTT-AAAGAGGCTATGCTCCAA 	13191
Query	953	GCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAGCTCTTGGG 	1010
Sbjct	13192	GCCCATCGCGC-ACACCAGCTGGCCAT-TGACACCTACCAGGAGTTTATAAGCTCTTGGG 	13249
Query	1011	TAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATG 	1069
Sbjct	13250	GAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGAAGTAATG 	13309
Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATA 	1129
Sbjct	13310	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAATGCAGGCAGATGAGCATA 	13369
Query	1130	CGCTGAGTGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT----AG-A-- 	1182
Sbjct	13370	GGCTGAGCCAGGTTCCCAGAAGAGTAACAGTGGGAGCTGGTCTCCAGCATAGAAAGCAGT 	13429
Query	1183	----C--CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATC-CTGAAGGAGCAGA 	1235
Sbjct	13430	GGTCTTCTTGGTGGGGGTCTTCCCCTAGGAAGAAGCCTATATCAC-AAAGGAACAGA 	13488
Query	1236	AGTATTCAATTCCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACA 	1294
Sbjct	13489	AGTATTCAATTCCTGCATG-ACTCCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACA 	13547
Query	1295	-CCTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGATGCCT-TCTCCCCAGG- 	1351
Sbjct	13548	TCC-TCCAACATGGAGGAAACGCAGCAGAAATCCGTGAGTGATG-CTGTCT-CCTAGGC 	13604
Query	1352	TGGGATGGGGTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTTCC 	1411
Sbjct	13605	GGGGATGGGGGAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCTTTCC 	13664
Query	1412	CCTGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCC 	1471
Sbjct	13665	CCTGCAGAACTTAGAGCTGCTCCACATCTCCCTGCTGCTCATCGAGTCGCGGCTGGAGCC 	13724
Query	1472	CGTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAA 	1531
Sbjct	13725	CGTGCGGTTCCTCAGGAGTACCTTACCAACAACCTGGTGTATGACACCTCGGACAGCGA 	13784
Query	1532	CGTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGT 	1591
Sbjct	13785	TGACTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAATGCTGATGGGGGTGAGGGT 	13844
Query	1592	GGCACCAGGA-TCC--AATCCTGGG-GCCCCACTGGCTTCCAGGGACTGGGG-AGAGAAA 	1646
Sbjct	13845	GGCACCAGGGGTCCCCAATCCTGGAAGCCC-ACTGGCTTCGAGGG-CTGGGGGAGAGAAA 	13902

Query	1647	CACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCA	1706
Sbjct	13903	CACTGCTGCCCTCTTTTCAGCAGTCAGGCGCTGACCCAAGAGAACTCACCATATTCTTCA	13962
Query	1707	TTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGG	1766
Sbjct	13963	TTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACA-CCTGAAGGGGAAGGAGGAAAATGG	14021
Query	1767	ATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCAC	1826
Sbjct	14022	ATAAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGTCTCTCCTTCTCTTGCTTCAC	14081
Query	1827	TTTGCAGAGGCTGGAAGATGGCAGCCCCCGACTGGGCAGATCTTCAATCAGTCTACAG	1886
Sbjct	14082	TTTGCAGAGGCTGGAAGACGGCAGCCACCTGACTGGGCAGACCCTCAAGCAGACCTACAG	14141
Query	1887	CAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTA	1946
Sbjct	14142	CAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCCA	14201
Query	1947	CTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGAGTGCCGCTC	2006
Sbjct	14202	CTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGAGTGCCGCTC	14261
Query	2007	TGTGGAGGGCAGCTGTGGCTTCTAGCTGCCC GGTTGGCATCCCTGTGACCCCTCCCCAGT	2066
Sbjct	14262	TGTGGAGGGCAGCTGTGGCTTCTAGGGGCCCGCTGGCATCC-TGTGACCCCTCCCCAGT	14320
Query	2067	GCCTCTCCTGGTTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATT	2126
Sbjct	14321	GCCTCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATT	14379
Query	2127	AAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA-GGCGGG	2185
Sbjct	14380	AAGTTGTATTGTTTCATCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGAAGGTGG-	14438
Query	2186	TGGTATGGAGCAAGGGGCCAGGTTGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCG	2245
Sbjct	14439	TGGTATGGAGCAAGGGGT-AGGT-GGGAAGACGACCTGGAGGGCCTTCAGGGTCTATT-G	14495
Query	2246	GGAACCAGGC 2255	
Sbjct	14496	GGAAC TAGGC 14505	

Score = 2920 bits (1581), Expect = 0.0
 Identities = 2065/2291 (90%), Gaps = 64/2291 (2%)
 Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATCATGCCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT	60
Sbjct	49740	GAATTCAGGACTCAATGGTGTCTAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT	49798
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	49799	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGGAGGAGGAAAG	49858
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA	180

Sbjct	49859	GAATAGGATAGAGAGTGGAATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA	49917
Query	181	TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCACGTGACCC	240
Sbjct	49918	GCCTTCCCCGCGTTTCAGGTTGACCAACATGGCCTGCAGCCAGAGGGCACCACCTGACCC	49977
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTA-TCTCTGGCTGACATTCTGTGCACAACCCTCACA	299
Sbjct	49978	TCAAAGAGAGGACAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGCACAATCCTTACA	50036
Query	300	ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT	359
Sbjct	50037	ACACTGGTGATGGTGAGAAGGGAAAGACGACAAGCCAGGGGGCATGATCCCAGCATGTGT	50096
Query	360	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACAT	419
Sbjct	50097	GGGAGGAGCTTCCAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	50156
Query	420	GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC	478
Sbjct	50157	ACACAGAAACAGGTGGGGTCAAGCAGGGAGAGAGAACTGGCCAGGGTATAAAAAGGGCCC	50216
Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGG	538
Sbjct	50217	ACAAGAGACCGGCTCTAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGG	50276
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCTAAAATCCCTTT-GGCACAAT	596
Sbjct	50277	ACAGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCTAAAAT-CCTTTGGGCACAAC	50335
Query	597	GTGTCCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	656
Sbjct	50336	GTGTCCTGAGGGGAGAGGCGGCGCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT	50395
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAG-TATTTGGCCAATCTCTGAATG	715
Sbjct	50396	GGGGCTTATGAATGTGAGC-ATCGCCATCTAAGGCCAGATATTTGGCCAATCTCTGAATG	50454
Query	716	TTCCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAAAAAACCAGCTCCTGGA	775
Sbjct	50455	TTCCTGGTCTCTGGA-G-GG-A-TG-GAGAGAGAGA-AAAAAACAAA--CAGCTCCTGGA	50506
Query	776	ACAGGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCC	834
Sbjct	50507	GCAGGGGAGAGCGCTGGCCTCTTCCTCTCCGGCTCCCTCCATTGCCCTCCGGTTTCTCCCC	50566
Query	835	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGA	894
Sbjct	50567	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGA	50626
Query	895	GGGC-AGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCG	953
Sbjct	50627	-GGCTGGTGCCGTCCAAACCGTTCCGTTATCCAGGCTTTTTGACCACGCTATGCTCCAAG	50685
Query	954	CCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGT	1011
Sbjct	50686	CCCATCGCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAGTTCTTGGGG	50743
Query	1012	AATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATGG	1070

Sbjct	50744	AATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTG-AC TT-CCCCACTGGGGAAGTAATGG	50801
Query	1071	GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATAC	1130
Sbjct	50802	GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAATGCAGGCAGATGAGCATAG	50861
Query	1131	GCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT-----AG-A	1182
Sbjct	50862	GCTGAGCCAGGTTCCCGAGAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACCAGCA	50921
Query	1183	---C--CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAG	1237
Sbjct	50922	GTCCTTCTTGGTGGGGGGTCTTCTCCTAGGAAGAAACCTATATCCCAAAGGACCAGAAG	50981
Query	1238	TATTCAATCCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACC	1296
Sbjct	50982	TATTCAATCCTGCATG-ACTCCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACACC	51040
Query	1297	TTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCC-AGG-TGG	1354
Sbjct	51041	CTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCCTAGGCGGG	51100
Query	1355	GATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCCCT	1414
Sbjct	51101	GATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGGTCTTCCCCCT	51160
Query	1415	GCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGT	1474
Sbjct	51161	GCAGAATCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCGT	51220
Query	1475	GCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGT	1534
Sbjct	51221	GCGGTTCTCCTCAGGAGTATGTTGCCAACAACTGGTGTATGACACCTCGGACAGCGATGA	51280
Query	1535	CTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGC	1594
Sbjct	51281	CTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGC	51340
Query	1595	ACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACACT	1650
Sbjct	51341	GCCAGGGGTGCGCAATCCTGGAACCCCCACTGGCTTAGAGGG-CTGGGGGAGAGAAACA-T	51398
Query	1651	GCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCAATTC	1710
Sbjct	51399	GCTGCCCTCTTTGTAGCAGTCAGGCGCTGACCCAAGAGAACTACCTTATTCTTCAATTC	51458
Query	1711	CCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGA	1770
Sbjct	51459	GCCTGGT-AATCCTCCAGGCCCTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGGATGA	51517
Query	1771	ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTG	1830
Sbjct	51518	ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTG	51577
Query	1831	CAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAG	1890
Sbjct	51578	CAGAGGCTGGAAGACGGCAGCCCGCGGACTGGGCAGATCCTCAAGCAGACCTACAGCAAG	51637
Query	1891	TTTGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC	1950

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Sbjct  51638  TTTGACACAAACTCACACAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC  51697
Query  1951    TTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTG  2010
          |||
Sbjct  51698  TTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGCAGTGCCGCTCTGTA  51757
Query  2011    GAGGGCAGCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACC--CC--TCCCCAGT  2066
          |||||
Sbjct  51758  GAGGGTAGCTGTGGCTTCTAGGTGCCCCGCGTGGCATCC-TGTGACCGACCCCTCCCCAGT  51816
Query  2067    GCCTCTCCTGGTTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATT  2126
          |||
Sbjct  51817  GCCTCTCCTGGCCCTGGAAGGTGCCACTCCAGTGCCCATCAGCCTTGTCTTAATAAAATT  51876
Query  2127    AAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA-GGCGGG  2185
          |||||
Sbjct  51877  AAGTTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGGAAGGTGG-  51935
Query  2186    TGGTATGGAGCAAGGGGCCAGGTTGGAAGACA-ACCTGTAGGGCCTTCAGGGTCTATTTC  2244
          |||
Sbjct  51936  TGGTATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAAGATCTATT-  51991
Query  2245    GGGAACCAGGC  2255
          |||||
Sbjct  51992  GGGAAGTAGGC  52002

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Score = 204 bits (110), Expect = 2e-48
 Identities = 213/261 (81%), Gaps = 14/261 (5%)
 Strand=Plus/Plus

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Query  2250    CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA  2307
          |||
Sbjct  40645    CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA  40704
Query  2308    GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TGCAAGACCAGG  2364
          |||
Sbjct  40705    GCGATTCTCCTGCCTCAGCCTCCC-AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG  40761
Query  2365    -CTCAGCTAATTTTGTATTTT-GGTAGAGACGGGGTTTACCATATTGGCCAGTCTGG  2422
          |
Sbjct  40762    AC-CAGCTAATTTTGTATTTT-TAGG-AGAGATGGAGTTTGGCATGTGGGTTAGCCTGG  40819
Query  2423    TCTC-CATCTCCTGACCTCAGGTAATCCGCCCCGCTCGGCCTCCCAAATTGCTGGGATTA  2481
          |||
Sbjct  40820    TCTTGCA-CTCCTGACCTTAAGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTA  40878
Query  2482    CAGGTATGAGCCACTGGGCCC  2502
          |||
Sbjct  40879    TAGGCATGAGCCACCGTGCCC  40899

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>gb|AC040958.20| Homo sapiens chromosome 17, clone RP11-630H24, complete sequence
 Length=26211

Score = 4806 bits (2602), Expect = 0.0
 Identities = 2650/2670 (99%), Gaps = 16/2670 (0%)
 Strand=Plus/Minus

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Query  1      GAATTCAGCACTGAATCATGCCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCT  60

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Sbjct	13097	 GAATTCAGCACTGAATCATGCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCTT	13038
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 	120
Sbjct	13037	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	12978
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 	180
Sbjct	12977	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA	12919
Query	181	TCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC 	240
Sbjct	12918	TCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	12859
Query	241	TTAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACAA 	300
Sbjct	12858	TTAAGAGAGGACAAGTTGGGTGGTATCTCT-GCTGACATTCTGTGCACAACCCTCACAA	12800
Query	301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG 	360
Sbjct	12799	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	12740
Query	361	GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG 	420
Sbjct	12739	GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG	12680
Query	421	CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCAGGTATAAAAAGGGCCCAC 	480
Sbjct	12679	CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCAGGTATAAAAAGGGCCCAC	12620
Query	481	AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC 	540
Sbjct	12619	AAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC	12560
Query	541	AGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTT-GGCACAATGT 	598
Sbjct	12559	AGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGGCACAATGT	12500
Query	599	GTCCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG 	658
Sbjct	12499	GTCCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTTGG	12440
Query	659	GGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTT 	718
Sbjct	12439	GGCTTATGAATGTTAG-TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTT	12381
Query	719	CTGGTCCCTGGA-GGAGGCAGAGAGAGAGAGAGAGAAAAAAAACCCAGCTCCTGGAAC 	777
Sbjct	12380	CTGGTCCCTGGAAGGGAGGCAGAGAGAGAGAGAGAG-AAAAAAAAACCCAGCTCCTGGAAC	12322
Query	778	AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCCAG 	836
Sbjct	12321	AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCCCTCCGGTTTCTCCCCAG	12262
Query	837	GCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGG 	896
Sbjct	12261	GCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGG	12202
Query	897	GCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTTGACAACGCTATGCTCCGCGCCC 	956

Sbjct	12201	 GCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTGGACAACGCTATGCTCCGCGCCC	12142
Query	957	GTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTAATGG	1016
Sbjct	12141	 GTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTAATGG	12082
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	12081	 GTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAAGTAATGGGAGGAG	12022
Query	1077	ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAG	1136
Sbjct	12021	 ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAG	11962
Query	1137	TGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGT	1196
Sbjct	11961	 TGAGGTTCCCGAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGT	11902
Query	1197	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAACC	1256
Sbjct	11901	 CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAACC	11842
Query	1257	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	1316
Sbjct	11841	 CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	11782
Query	1317	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGT-GGGATGGGGTAGACCTGTGGTCA	1375
Sbjct	11781	 AGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGGGTAGGGTAGACCTGTGGTCA	11722
Query	1376	GAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAACCTAGAGCTGCTCCG	1435
Sbjct	11721	 GAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAACCTAGAGCTGCTCCG	11662
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	1495
Sbjct	11661	 CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	11602
Query	1496	CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCT	1555
Sbjct	11601	 CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCT	11542
Query	1556	AGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA-GGAT--CCAATCCTGG	1612
Sbjct	11541	 AGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAAGGGATCCCCAATCCTGG	11482
Query	1613	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTAGCAGTCA	1672
Sbjct	11481	 GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTAGCAGTCA	11422
Query	1673	GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCT	1732
Sbjct	11421	 GGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCT	11362
Query	1733	TTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTG	1792
Sbjct	11361	 TTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTG	11302
Query	1793	CCCAAGCGCTTGGCCTCTCCTTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCC	1852

Sbjct	11301	 CCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCC	11242
Query	1853	CCCCGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG	1912
Sbjct	11241	 CCCCGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG	11182
Query	1913	ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG	1972
Sbjct	11181	 ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG	11122
Query	1973	TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC	2032
Sbjct	11121	 TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC	11062
Query	2033	TGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTA	2092
Sbjct	11061	 TGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGTGCTA	11002
Query	2093	CTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGGTACTAGG	2152
Sbjct	11001	 CTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTGGTACTAGG	10942
Query	2153	TGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGG	2212
Sbjct	10941	 TGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGC-AGGTTGGG	10883
Query	2213	AAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGAACACAGGCTGGAGTGCAGTGGCA-G	2271
Sbjct	10882	 AAGACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACACAGGCTGGAGTGCAGTGGCACG	10824
Query	2272	-TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCC	2330
Sbjct	10823	 ATCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCC	10764
Query	2331	CGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA	2390
Sbjct	10763	 CGAATAGTTGGGATTCCAGGCATGCACGACCAGGCTCAGCTAATTTTTGTATTTTTGGTA	10704
Query	2391	GAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCG	2450
Sbjct	10703	 GAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCG	10644
Query	2451	CCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT	2510
Sbjct	10643	 CCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGT	10584
Query	2511	CCTGTGATTTTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT	2570
Sbjct	10583	 CCTGTGATTTTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCT	10524
Query	2571	GGCCATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATT	2630
Sbjct	10523	 GGCCATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATT	10464
Query	2631	GGGTCCACTCAGTAGATGCTTGTTGAATTC	2660
Sbjct	10463	 GGGTCCACTCAGTAGATGCTTGTTGAATTC	10434

Query	835	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGA	894
Sbjct	4083	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGA	4024
Query	895	GGGC-AGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCG	953
Sbjct	4023	-GGCTGGTGCCGTCCAAACCGTTCCGTTATCCAGGCTTTTTGACCACGCTATGCTCCAAG	3965
Query	954	CCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGT	1011
Sbjct	3964	CCCATCGCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAGTTCTTGGGG	3907
Query	1012	AATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATGG	1070
Sbjct	3906	AATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGAAGTAATGG	3847
Query	1071	GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATAC	1130
Sbjct	3846	GAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAATGCAGGCAGATGAGCATAG	3787
Query	1131	GCTGAGTGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT-----AG-A	1182
Sbjct	3786	GCTGAGCCAGGTTCCCAGAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACCAGCA	3727
Query	1183	---C--CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAG	1237
Sbjct	3726	GTCCTTCTTGGTGGGGGTCTTCTCCTAGGAAGAAACCTATATCCCAAAGGACCAGAAG	3667
Query	1238	TATTCATTCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACC	1296
Sbjct	3666	TATTCATTCTGTCATG-ACTCCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACACC	3608
Query	1297	TTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCC-AGG-TGG	1354
Sbjct	3607	CTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCCTAGGCGGG	3548
Query	1355	GATGGGGTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCT	1414
Sbjct	3547	GATGGGGGAGACCTGTGGTCAGGGCTCCCGGCAGCACAGCCACTGCCGGTCCTTCCCCT	3488
Query	1415	GCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCCT	1474
Sbjct	3487	GCAGAATCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCCT	3428
Query	1475	GCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGT	1534
Sbjct	3427	GCGGTTCTCAGGAGTATGTTTCGCCAACAACTGGTGTATGACACCTCGGACAGCGATGA	3368
Query	1535	CTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGC	1594
Sbjct	3367	CTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGC	3308
Query	1595	ACCA-GGAT--CCAATCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACACT	1650
Sbjct	3307	GCCAGGGGTGCGCAATCTTGAACCCCACTGGCTTAGAGGG-CTGGGGGAGAGAAACACT	3249
Query	1651	GCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTT	1710
Sbjct	3248	GCTGCCCTCTTTGTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCTTATTCTTCATTTT	3189

Query	1711	CCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGA	1770
Sbjct	3188	GCCTGGTGAATCCTCCAGGCCCTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGGATGA	3129
Query	1771	ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTG	1830
Sbjct	3128	ATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTG	3069
Query	1831	CAGAGGCTTGAAGATGGCAGCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAG	1890
Sbjct	3068	CAGAGGCTTGAAGACGGCAGCCGCCGGACTGGGCAGATCCTCAAGCAGACCTACAGCAAG	3009
Query	1891	TTTGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC	1950
Sbjct	3008	TTTGACACAAACTCACACAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGC	2949
Query	1951	TTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTG	2010
Sbjct	2948	TTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGCAGTGCCGCTCTGTA	2889
Query	2011	GAGGGCAGCTGTGGCTTCTAGCTGCCCGGTGGCATCCCTGTGACC--CC--TCCCCAGT	2066
Sbjct	2888	GAGGGTAGCTGTGGCTTCTAGGTGCCCGCGTGGCATCC-TGTGACCGACCCCTCCCCAGT	2830
Query	2067	GCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGTCTAATAAAATT	2126
Sbjct	2829	GCCTCTCCTGGCCCTGGAAGGTGCCACTCCAGTGCCCATCAGCCTTGTCTAATAAAATT	2770
Query	2127	AAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGG-GGCGGG	2185
Sbjct	2769	AAGTTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGGGAGGTGG-	2711
Query	2186	TGGTATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCTATTC	2244
Sbjct	2710	TGGTATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAAGGTCTATT-	2655
Query	2245	GGGAACCAAGGC	2255
Sbjct	2654	GGGAACCAAGGC	2644

Score = 941 bits (509), Expect = 0.0
 Identities = 622/675 (92%), Gaps = 14/675 (2%)
 Strand=Plus/Minus

Query	1587	AGGGTGGCACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGA	1642
Sbjct	26211	AGGGTGGCGCCAGGGGTACCAATCCTGGAACCCCACTGGCTTCGAGGG-CTGGGGGAGA	26153
Query	1643	GAAACACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTC	1702
Sbjct	26152	GAAATACTGCTGCCCTCTTTTTAGCAGTAAGGCGCTGACCCAAGAGAACTACCTTATTC	26093
Query	1703	TTCATTTCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAA	1762
Sbjct	26092	TTCATTTGCGCTGGTGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAA	26033
Query	1763	ATGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCT	1822
Sbjct	26032	ATGGATAAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCT	25973

Query	1823	TCAC TTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCT	1882
Sbjct	25972	TCAC TTTGCAGAGGCTGGAAGACGGCAGCCCGGACTGGGCAGATCCTCAAGCAGACCT	25913
Query	1883	ACAGCAAGTTTGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGCTGC	1942
Sbjct	25912	ACAGCAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCTGC	25853
Query	1943	TCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGAGTGCC	2002
Sbjct	25852	TCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGAGTGCC	25793
Query	2003	GCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCC	2062
Sbjct	25792	GCTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCCGAGTAGCATCC-TGTGACCCCTCCC	25734
Query	2063	CAGTGCCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAA	2122
Sbjct	25733	CAGTGCCCTCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCCACCAGCCTTGTCTTAATAA	25675
Query	2123	AATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA-GG	2181
Sbjct	25674	AATTAAGTTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGGAAGG	25615
Query	2182	CGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCT	2240
Sbjct	25614	TGG-TGGTATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAAGGTCT	25559
Query	2241	ATTCGGAACCAAGGC	2255
Sbjct	25558	ATT-GGGAAGTAGGC	25545

Score = 209 bits (113), Expect = 5e-50
 Identities = 213/260 (81%), Gaps = 12/260 (4%)
 Strand=Plus/Minus

Query	2250	CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA	2307
Sbjct	14047	CCAGGCTGGAGTGCAGTGGCGCAATCTTGGCTCACAGCAACCTCTGCCTCCTGGGTTCAA	13988
Query	2308	GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TGCAAGACCAGG	2364
Sbjct	13987	GCGATTCTCCTGCCTCAGCCTCCC-AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG	13931
Query	2365	CTCAGCTAATTTTTGTATTTTT-GGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGT	2423
Sbjct	13930	CCCAGCTAATTTTTGTATTTTTAGG-AGAGATGGAGTTTTGCCATGTGGGTTAGCCTGGT	13872
Query	2424	CTC-CATCTCCTGACCTCAGGTAATCCGCCCCGCTCGGCCTCCCAAATTGCTGGGATTAC	2482
Sbjct	13871	CTTGCA-CTCCTGACCTTAAGTGATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTAT	13813
Query	2483	AGGTATGAGCCACTGGGCCC	2502
Sbjct	13812	AGGCATGAGCCACCGTGCCC	13793

>gb|EU421715.1| Homo sapiens growth hormone 2 precursor (GH2) gene, complete

Sbjct	777	 CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTGTGACAACG	836
Query	942	CTATGCTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAA	1001
Sbjct	837	 CTATGCTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAA	896
Query	1002	GCTCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGG	1061
Sbjct	897	 GCTCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGG	956
Query	1062	AAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGA	1121
Sbjct	957	 AAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGA	1016
Query	1122	TGAGCATACGCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAG	1181
Sbjct	1017	 TGAGCATACGCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAG	1076
Query	1182	ACCTTGGTGGGCGGTCCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATT	1241
Sbjct	1077	 ACCTTGGTGGGCGGTCCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATT	1136
Query	1242	CATTCTGCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCA	1301
Sbjct	1137	 CATTCTGCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCA	1196
Query	1302	ACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGT-GGGATGGG	1360
Sbjct	1197	 ACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGG	1256
Query	1361	GTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAA	1420
Sbjct	1257	 GTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAA	1316
Query	1421	CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCT	1480
Sbjct	1317	 CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCT	1376
Query	1481	CCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCG	1540
Sbjct	1377	 CCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCG	1436
Query	1541	CCACCTGAAGGACCTAGAGGAAGGCATCAAACGCTGATGTGGGTGAGGGTGGCACCA-G	1599
Sbjct	1437	 CCACCTGAAGGACCTAGAGGAAGGCATCAAACGCTGATGTGGGTGAGGGTGGCACCAAGG	1496
Query	1600	GAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCC	1657
Sbjct	1497	 GATCCCCAATCCTGGGGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCC	1556
Query	1658	TCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCCTCGT	1717
Sbjct	1557	 TCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCATTTCCCCTCGT	1616
Query	1718	GAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAG	1777
Sbjct	1617	 GAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAG	1676
Query	1778	AGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGC	1837

Sbjct	1677	 AGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGC	1736
Query	1838	TGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACA	1897
Sbjct	1737	 TGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACA	1796
Query	1898	CAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGA	1957
Sbjct	1797	 CAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGA	1856
Query	1958	AGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCA	2017
Sbjct	1857	 AGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCA	1916
Query	2018	GCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGG	2077
Sbjct	1917	 GCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGG	1976
Query	2078	TCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCA	2137
Sbjct	1977	 TCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCA	2036
Query	2138	TTTTGTTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCA	2197
Sbjct	2037	 TTTTGTTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCA	2096
Query	2198	AGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGAACCAGGCTG	2257
Sbjct	2097	 AGGGGC-AGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACCAGGCTG	2154
Query	2258	GAGTGCAGTGGCA-G-TCTTGGCTCGCTGCAATCTCCGCC	2295
Sbjct	2155	 GAGTGCAGTGGCACGATCTTGGCTCGCTGCAATCTCCGCC	2194

>gb|AC127029.12| Homo sapiens chromosome 17, clone CTC-264K15, complete sequence
Length=101990

Score = 3864 bits (2092), Expect = 0.0
Identities = 2487/2675 (92%), Gaps = 37/2675 (1%)
Strand=Plus/Minus

Query	1	GAATTCAGCACTGAATCATGCCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT	60
Sbjct	28460	 GAATTCAGGACTGAATCGTGCTCACAACCCCAACAATCTATTGGCTGTGC-TTGGCCCT	28402
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	28401	 TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG	28342
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTA-GGGGTCTCAAGGACTGGCCTATCCTGAC	179
Sbjct	28341	 GGATAGGATAGAGAATGGGATGTGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGAC	28283
Query	180	ATCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACC	239
Sbjct	28282	 ATCCTTCGCCGCGTGACAGGTTGGCCACCATGGCCTGCGGCCAGAGGGCACCCACGTGACC	28223
Query	240	CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACA	299

Sbjct	27338	 AGTGAGGTTCCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGACCTTGGTGGGCG	27279
Query	1195	GTCCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAA	1254
Sbjct	27278	 GTCCTTCTCCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGTATTCATTCTGCAGAA	27219
Query	1255	CCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAAC	1314
Sbjct	27218	 CCCCCAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCCTCCAACAGGGAGGAAAC	27159
Query	1315	GCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGG-TGGGATGGGGTAGACCTGTGGT	1373
Sbjct	27158	 ACAACAGAAATCCGTGAGTGGATGCCTTCTCCCCAGGCGGGGATGGGGGAGACCTGTAGT	27099
Query	1374	CAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAACCTAGAGCTGCTC	1433
Sbjct	27098	 CAGAGCCCCCGGGCAGCACAGCCAATGCCCGTCCTTCCCCTGCAGAACCTAGAGCTGCTC	27039
Query	1434	CGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTC	1493
Sbjct	27038	 CGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTTCCTCAGGAGTGTC	26979
Query	1494	TTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCG-CCACCTGAAGGA	1552
Sbjct	26978	 TTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTAT-GACCTCTAAAGGA	26920
Query	1553	CCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA-GGAT--CCAATCC	1609
Sbjct	26919	 CCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCC	26860
Query	1610	TGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGCTGCCCTCTTTTATGCA	1668
Sbjct	26859	 TGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGCTGCCCTCTTTTATGCA	26801
Query	1669	GTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCAATTTCCCCTCGTGAATCCTCCAG	1728
Sbjct	26800	 GTCAGGCCCTGACCCAAGAGAACTACCTTATTCTTCAATTTCCCCTCGTGAATCCTCCAG	26741
Query	1729	GCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAAC	1788
Sbjct	26740	 GCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGAATGAATGAGAAAGGGAGGGAAC	26681
Query	1789	AGTGCCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGC	1848
Sbjct	26680	 AGTACCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGC	26621
Query	1849	AGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCAC	1908
Sbjct	26620	 AGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACAC	26561
Query	1909	AACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	1968
Sbjct	26560	 AACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGAC	26501
Query	1969	AAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC	2028
Sbjct	26500	 AAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTC	26441
Query	2029	TAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCGTGGAAGGT	2088

Sbjct	26440	 TAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTT	26381
Query	2089	GCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTTGAC	2148
Sbjct	26380	 GCCACTCCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTTGAC	26321
Query	2149	TAGGTGTCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGT	2208
Sbjct	26320	 TAGGTGTCTTCTATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCAAG-T	26262
Query	2209	TGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGAACCAGGCTGGAGTGCAGTGG	2268
Sbjct	26261	 TGGGAAGACAACCTGTAGGGCCTGCGGGGTCTATT-GGGAACCAAGCTGGAGTGCAGTGG	26203
Query	2269	CAG--TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGT	2326
Sbjct	26202	 CACAATCTTGGCTCACTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGC	26143
Query	2327	CTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTGTATTTT	2386
Sbjct	26142	 CTCCCGAGTTGTTGGGATTCCAGGCATGCATGACCAGGCTCAGCTAATTTTGTTTTTT	26083
Query	2387	GGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAA	2446
Sbjct	26082	 GGTAGAGACGGGGTTTCACCATATTGGCCAGGCTGGTCTCCAACCTCCTAATCTCAGGTGA	26023
Query	2447	TCCGCCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCC	2506
Sbjct	26022	 TCTACCCACCTTGGCCTCCCAAATTGCTGGGATTACAGGCGTGAACCACTGCTCCCTTCC	25963
Query	2507	CTGTCCTG-TGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGC	2565
Sbjct	25962	 CTGTCCTTCTGATTTTAAAATAACTATACCAGCAGGAGGACGTCCAGACACAGCATAGGC	25903
Query	2566	TACCTGGCCATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCAT	2625
Sbjct	25902	 TACCTGGCCATGCCCAACCGGTGGGACATTTGAGTTGCTTGGCACTGTCCTCTCAT	25843
Query	2626	GCATTGGGTCCACTCAGTAGATGCTTGTGAATTC	2660
Sbjct	25842	 GCGTTGGGTCCACTCAGTAGATGCCTGTTGAATTC	25808

Score = 2987 bits (1617), Expect = 0.0
Identities = 2074/2288 (90%), Gaps = 57/2288 (2%)
Strand=Plus/Minus

Query	1	GAATTCAGCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT	60
Sbjct	6195	 GAATTCAGGACTCAATGGTGTCTAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT	6137
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	6136	 TTTCCCAACACACACATTCTGTCTGGTGGGTGGAAGTTAAACACGCGGGGAGGAGGAAAG	6077
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGACA	180
Sbjct	6076	 GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGACA	6018

Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATA	1129
Sbjct	5130	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAATGCAGGCAGATGAGCATA	5071
Query	1130	CGCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT-----AG-	1181
Sbjct	5070	GGCTGAGCCAGGTTCCCGAGAAAAGCAACAATGGGAGCTGGTCTCCAGCATAGAAACCAGC	5011
Query	1182	A---C--CTTGGTGGGCGGTCTTCTCTCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAA	1236
Sbjct	5010	AGTCCTTCTTGGTGGGGGGTCTTCTCTCTAGGAAGAAACCTATATCCCAAAGGACCAGAA	4951
Query	1237	GTATTCATTCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACAC	1295
Sbjct	4950	GTATTCATTCTGTCATG-ACTCCCAGACCTCTTCTGCTTCTCAGACTCTATTCCGACAC	4892
Query	1296	CTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCC-AGG-TG	1353
Sbjct	4891	CCTCCAACATGGAGGAAACGCAACAGAAATCCGTGAGTGGATGCCGTCTCCCCTAGGCGG	4832
Query	1354	GGATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTCCCC	1413
Sbjct	4831	GGATGGGGGAGACCTGTGGTCAGGGCTCCCGGGCAGCACAGCCACTGCCGGTCTTCCCC	4772
Query	1414	TGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCG	1473
Sbjct	4771	TGCAGAATCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCTGGAGCCCG	4712
Query	1474	TGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACG	1533
Sbjct	4711	TGCGGTTCTCTCAGGAGTATGTTTCGCCAACAACTGGTGTATGACACCTCGGACAGCGATG	4652
Query	1534	TCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGG	1593
Sbjct	4651	ACTATCACCTCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGG	4592
Query	1594	CACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAGAAACAC	1649
Sbjct	4591	CGCCAGGGGTACCAATCCTGGAACCCCACTGGCTTCGAGGG-CTGGGGGAGAGAAATAC	4533
Query	1650	TGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTACCGTATTCTTCAATTT	1709
Sbjct	4532	TGCTGCCCTCTTTTTAGCAGTAAGGCGCTGACCCAAGAGAACTACCTTATTCTTCAATTT	4473
Query	1710	CCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATG	1769
Sbjct	4472	CGCCTGGTGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGGATA	4413
Query	1770	AATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTT	1829
Sbjct	4412	AATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTT	4353
Query	1830	GCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCTACAGCAA	1889
Sbjct	4352	GCAGAGGCTGGAAGACGGCAGCCCGCGGACTGGGCAGATCCTCAAGCAGACCTACAGCAA	4293
Query	1890	GTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTG	1949
Sbjct	4292	GTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTG	4233

Query	1950	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAAGTCCGCTCTGT	2009
Sbjct	4232	CTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGCAAGTCCGCTCTGT	4173
Query	2010	GGAGGGCAGCTGTGGCTTCTAGCTGCCCAGGTGGCATCCCTGTGACCCCTCCCCAGTGCC	2069
Sbjct	4172	GGAGGGCAGCTGTGGCTTCTAGGTGCCCAGTAGCATCC-TGTGACCCCTCCCCAGTGCC	4114
Query	2070	TCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCAGCCTTGTCTAATAAAATTAAG	2129
Sbjct	4113	TCTCCTGGCCCTG-AAGGTGCCACTCCAGTGCCACCAGCCTTGTCTAATAAAATTAAG	4055
Query	2130	TTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA-GGCGGGTGG	2188
Sbjct	4054	TTGTATCATTTTCATCTGACTAGGTGTCATTCTATAATATTATGGGGTGGAAGGTGG-TGG	3996
Query	2189	TATGGAGCAAGGGGCCAGGTTGGGAAGACA-ACCTGTAGGGCCTTCAGGGTCTATTCTGGG	2247
Sbjct	3995	TATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTCAAGGTCTATT-GGG	3940
Query	2248	AACCAGGC 2255	
Sbjct	3939	AACTAGGC 3932	
Score = 2966 bits (1606), Expect = 0.0			
Identities = 2074/2291 (90%), Gaps = 68/2291 (2%)			
Strand=Plus/Minus			
Query	1	GAATTCAGCACTGAATCATGCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT	60
Sbjct	20879	GAATTCAGGACTGAATCATGCTCACAACCCCCACAATCTATTGGCTGTGC-TTGGCCCCCT	20821
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	20820	TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGTTAAACATGCGGGGAGGAGGAAAG	20761
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCTGACA	180
Sbjct	20760	GAATAGGATAGAGAGTGGGATGTGGTCGATAGGGGTCTCAAGGACTGG-CTATCTGACA	20702
Query	181	TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	20701	TCCTTCTCCGCATTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACCTGAACC	20642
Query	241	TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACAA	300
Sbjct	20641	TTAAAGAGAGGACAAGTTGGGTGGTGTCTGTGGTTGACACTCTGTGCACAACCCTCACAA	20582
Query	301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	360
Sbjct	20581	CGCTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGACATGATGCCAGCATGTGTG	20522
Query	361	GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG	420
Sbjct	20521	GGAGGAGCTTCCAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGTG	20462
Query	421	CAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCC	478
Sbjct	20461	CACAGAAACAGGTG-GGGGCAA-CAGCGAGAGAGAAGGGGCCAGGGTATAAAAAGGGCCC	20404

Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCAACTCCCCGAACCACTCAGGGTCCTGTGG 	538
Sbjct	20403	ACAAGAGACCAGCTCCAGCATCCCAAGGCCCGACTCCCCGCACCACTCAGGGTCCTGTGG 	20344
Query	539	ACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTT-GGCACAAT 	596
Sbjct	20343	ACAGCTCACCTAGCGGCAATGGCTGCAGGTAAGCGCCCCATAAATCCCTTTGGGCACAAC 	20284
Query	597	GTGTCTTGAGGGGAGAGGCGGCGTCTGTAGATGGGACGGGGGCACTAACCCCTCAGGTTT 	656
Sbjct	20283	GTGTCTTGAGGGGAGAGGCGGCGCCTTGCAGATGGGACGGGGGCACTAA-CCTCAGGTTT 	20225
Query	657	GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAG-TATTGGCCAATCTCTGAATG 	715
Sbjct	20224	GGGGCTTCTGAATGTGA-ATATCGCCATCTAAGGCCAGATATTGGCCAATCTCTGAATG 	20166
Query	716	TTCCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAAAAAAAACCCAGCTCCTGGA 	775
Sbjct	20165	TTCCTGGTCCCT---GGAGG--GA-TG-GAGAGAGAGAAAAAGAAAA--CAGCTCCTGGA 	20115
Query	776	ACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCCCC 	834
Sbjct	20114	ACAGGGAGAGTGCTGGCCTCTTGCTCTGCGGCTCCCT-TCTTGCCCTCCGGTTTCTCCCC 	20056
Query	835	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTTGCTTCAAGA 	894
Sbjct	20055	AGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCTTGCTTCAAGA 	19996
Query	895	GGGC-AGTGCCTTCCCAACCATTTCCCTTATCCAGGCTTTTTTGACA-ACGCTATGCTCCGC 	952
Sbjct	19995	-GGCTGGTGCCGTCCAAACCGTTCCCTTATCCAGGCTTTTT-AAAGAGGCTATGCTCCAA 	19938
Query	953	GCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAGCTCTTGGG 	1010
Sbjct	19937	GCCCATCGCGC-ACACCAGCTGGCCAT-TGACACCTACCAGGAGTTATAAGCTCTTGGG 	19880
Query	1011	TAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATG 	1069
Sbjct	19879	GAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGAAGTAATG 	19820
Query	1070	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATA 	1129
Sbjct	19819	GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGCGAAAATGCAGGCAGATGAGCATA 	19760
Query	1130	CGCTGAGTGAGGTTCCCAAGAAAGTAACAATGGGAGCAGGTCTCCAGCAT----AG-A-- 	1182
Sbjct	19759	GGCTGAGCCAGGTTCCCAAGAGTAACAGTGGGAGCTGGTCTCCAGCATAGAAAGCAGT 	19700
Query	1183	----C--CTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATC-CTGAAGGAGCAGA 	1235
Sbjct	19699	GGTCCTTCTTGGTGGGGGTCTTCCCTTAGGAAGAAGCCTATATCAC-AAAGGAACAGA 	19641
Query	1236	AGTATTCATTCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACA 	1294
Sbjct	19640	AGTATTCATTCTGCATG-ACTCCCAGACCTCCTTCTGCTTCTCAGACTCTATTCCGACA 	19582
Query	1295	-CCTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCT-TCTCCCC-AGG 	1351
Sbjct	19581	TCC-TCCAACATGGAGGAAAACGCAGCAGAAATCCGTGAGTGGATG-CTGTCTCCCCTAGG 	19521

Query	1352	-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTC	1410
Sbjct	19523	CGGGGATGGGGGAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTC	19464
Query	1411	CCCTGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGC	1470
Sbjct	19463	CCCTGCAGAACTTAGAGCTGCTCCACATCTCCCTGCTGCTCATCGAGTCGCGGCTGGAGC	19404
Query	1471	CCGTGCAGCTCCTCAGGAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCA	1530
Sbjct	19403	CCGTGCGGTTCTCAGGAGTACCTTCACCAACAACCTGGTGTATGACACCTCGGACAGCG	19344
Query	1531	ACGTCTATCGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGG	1590
Sbjct	19343	ATGACTATCACCTCCTAAAGGACCTAGAGGAAGGCATCCAAATGCTGATGGGGGTGAGGG	19284
Query	1591	TGGCACCA--GGAT--CCAATCCTGG--GGCCCCACTGGCTTCCAGGGACT--GGGGAGAGAA	1645
Sbjct	19283	TGGCACCAAGGGTCCCCAATCCTGGAAG--CCCACTGGCTTCGAGGG--CTGGGGGAGAGAA	19226
Query	1646	ACACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTC	1705
Sbjct	19225	ACACTGCTGCCCTCTTTTCAGCAGTCAGGCGCTGACCCAAGAGAACTCACCTTATTCTTC	19166
Query	1706	ATTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATG	1765
Sbjct	19165	ATTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGGGAAGGAGGAAAATG	19106
Query	1766	GATGAATGAGAGAGGGAGGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCA	1825
Sbjct	19105	GATAAATGAGAGAGGGAGGGGAACAGTGCCCAAGCGCTTGGTCTCTCCTTCTCTTGCTTCA	19046
Query	1826	CTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACA	1885
Sbjct	19045	CTTTGCAGAGGCTGGAAGACGGCAGCCACCTGACTGGGCAGACCCTCAAGCAGACCTACA	18986
Query	1886	GCAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCT	1945
Sbjct	18985	GCAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCTGCTCC	18926
Query	1946	ACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCT	2005
Sbjct	18925	ACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGGTGCAGTGCCGCT	18866
Query	2006	CTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCAGGTGGCATCCCTGTGACCCCTCCCCAG	2065
Sbjct	18865	CTGTGGAGGGCAGCTGTGGCTTCTAGGGGCCCCGCTGGCATCC--TGTGACCCCTCCCCAG	18807
Query	2066	TGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAAAT	2125
Sbjct	18806	TGCCTCTCCTGGCCCTG--AAGGTGCCACTCCAGTGCCCACCAGCCTTGTCTTAATAAAAT	18748
Query	2126	TAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGG--GGCGG	2184
Sbjct	18747	TAAGTTGTATTGTTTCATCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGGAAGGTGG	18688
Query	2185	GTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTC	2244
Sbjct	18687	-TGGTATGGAGCAAGGGGT--AGGT--GGGAAGACGACCTGGAGGGCCTTCAGGGTCTATT-	18632

Query	2250	CCAGGCTGGAGTGCAGTGGCA-G-TCTTGGCTCGCTGCAATCTCCGCCCTCTGGGTTCAA 	2307
Sbjct	33546	CCAGGCTAGAGTGCAATGGCACGATCTTGGCTCACTGCACCCTCCACCTCTGGGTTCAA	33487
Query	2308	GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCATGCAAGACCAGGCT 	2366
Sbjct	33486	GCGATTCTCCTGCCTCAGCCTCTC-AAGTAGCTGGGATTACAAGCGCCCCTACCAGGCT	33428
Query	2367	CAGCTAATTTTTGTATTTTTGGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTC 	2426
Sbjct	33427	CCGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATATTGGCCAGGCTGGTCTC	33368
Query	2427	CATCTCCTGACCTCAGGTAATCCGCCCGCCTCGGCCCTCCCAAATTGCTGGGATTACAGGT 	2486
Sbjct	33367	CAACTCCTGACCTCAGGTGATCCGCCCGCCTCGGCCCTCCCAAATTGCTGGGATCAGAGT	33308
Query	2487	ATGAGCCACTGGGCCCTTCCCTGTCCT-GTGATTTTAAAAATAATTATACCAGCAGAAGGA 	2545
Sbjct	33307	GTAAGCCACTGCGCCCTTCCCTGTCCTTGTCATTTTAAAAATAATTATACCAGCAGGAGGA	33248
Query	2546	CGTCCAGACACAGCATGGGCTACCTGGCCATGCCCAGCCAGTTGGACATTTGAGTTGTTT 	2605
Sbjct	33247	CGTCCAGACACAGCATGGGCTACCTGGCCATGCCCAGCTGGTTGGACATTTGAGTTCTTT	33188
Query	2606	GCTTGGCACTGTCCTCTCATGCATTGGGTCCACTCAGTAGATGCTTGTTGAATTC 	2660
Sbjct	33187	GCTTGGCACTGTCCTCTCATGCGTTGGGTCCACTCAGTAGATGCTTATTGAATTC	33133

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Sbjct	717	GCTCCTGGCTCCCT-----GG-AG-GA-TG-GAGAGAG-AAAAACAAA--CAGCTCCTG	763
Query	774	GAACAGGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGGTTTCTCC	832
Sbjct	764	GAGCAGGGGAGAGTGTGGCCTCTTGCTCTCCGGCTCCCTCTGTTGCCCTCTGGTTTCTCC	823
Query	833	CCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAA	892
Sbjct	824	CCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAA	883
Query	893	GAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTGTACAACGCTATGCTCCGC	952
Sbjct	884	GAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTGTACAACGCTATGCTCCGC	943
Query	953	GCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTA	1012
Sbjct	944	GCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGTAAGCTCTTGGGGA	1003
Query	1013	ATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCGCTGGGAAGTAATG-GG	1071
Sbjct	1004	ATGGGTGCGCATCAGGGGTGGCAGGAAGGGGTGACTTTCCCCGCT-GGAAATAA-GAGG	1061
Query	1072	AGGAGACTAAGGAGCTCAGGGTTGTTTTCTGA-AGTGAAAATGCAGGCAGATGAGCATAC	1130
Sbjct	1062	AGGAGACTAAGGAGCTCAGGGTT-TTCCCGACCGGAAAATGCAGGCAGATGAGCACAC	1120
Query	1131	GCTGAG-TGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT-AGACCTTGG	1188
Sbjct	1121	GCTGAGCT-AGGTTCCCAGAAAAGTAA-AATGGGAGCAGGTCT-CAGC-TCAGACCTTGG	1176
Query	1189	TGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCAATCCT	1248
Sbjct	1177	TGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGTATTCAATCCT	1236
Query	1249	GCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGT	1308
Sbjct	1237	GCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCTTCCAACAGGGA	1296
Query	1309	GAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGG-TGGGATGGGGTAGACC	1367
Sbjct	1297	GGAAACACAACAGAAATCCGTGAGTGGATGCCTTCTCCCCAGGCGGGGATGGGGGAGACC	1356
Query	1368	TGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTT-CCCCTGCAGAACCTAGA	1426
Sbjct	1357	TGTAGTCAGAGCCCCCGGGCAGCACAGCCAATGCCCGTCTTGCCCCCTGCAGAACCTAGA	1416
Query	1427	GCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGTCTCTCAG	1486
Sbjct	1417	GCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCAGTCTCTCAG	1476
Query	1487	GAGCGTCTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCG-CCACC	1545
Sbjct	1477	GAGTGTCTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTAT-GACCTCC	1535
Query	1546	TGAAGGACCTAGAGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCA-GGAT--	1602
Sbjct	1536	TAAAGGACCTAGAGGAAGGCATCCAACGCTGATGGGGGTGAGGGTGGCGCCAGGGGTCC	1595
Query	1603	CCAATCTGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACT-GCTGCCCTCT	1660

Sbjct	1596	 CCAATCCTGGAGCCCCACTGACTTTGAGAGACTGTGTTAGAGAAACACTGGCTGCCCTCT	1655
Query	1661	TTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAA	1720
Sbjct	1656	 TTTTAGCAGTCAGGCCCTGACCCAAGAGAACTCACCTTATTCTTCATTTCCCCTCGTGAA	1715
Query	1721	TCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGG	1780
Sbjct	1716	 TCCTCCAGGCCTTTCTCTAC-A-CTGAAGGGGAGGGAGGAAAATGAATGAATGAGAAAGG	1773
Query	1781	GAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGCTGG	1840
Sbjct	1774	 GAGGGAACAGTACCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCAGAGGCTGG	1833
Query	1841	AAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAA	1900
Sbjct	1834	 AAGATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTTTCGACACAA	1893
Query	1901	AATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGG	1960
Sbjct	1894	 ACTCACACAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGG	1953
Query	1961	ACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCT	2020
Sbjct	1954	 ACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCT	2013
Query	2021	GTGGCTTCTAGCTGCCCAGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGTCG	2080
Sbjct	2014	 GTGGCTTCTAGCTGCCCAGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCCC	2073
Query	2081	TGGAAGGTGCTACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATCATTT	2140
Sbjct	2074	 TGGAAGTTGCCACTCCAGTGCCCAACAGCCTTGTCTTAATAAAATTAAGTTGCATCATTT	2133
Query	2141	TGTTTACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGG	2200
Sbjct	2134	 TGTCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGG	2193
Query	2201	GGCC-AGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTTCGGAACCAAGGCTGGA	2259
Sbjct	2194	 GGCCCAAGTTGGGAAGACAACCTGTAGGGCCTGCGGGTCTATTTCGGAACCAAGGCTGGA	2253
Query	2260	GTGCAGTGGCAG--TCTTGGCTCGCTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCC	2317
Sbjct	2254	 GTGCAGTGGCACAATCTTGGCTCACTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCC	2313
Query	2318	TGCCTCAGTCTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTT	2377
Sbjct	2314	 TGCCTCAGCCTCCCGAGTTGTTGGGATTCCAGGCATGCATGACCAGGCTCAGCTAATTTT	2373
Query	2378	TGTATTTTTGGTAGAGACGGGGTTTACCATAATTGGCCAGTCTGGTCTCCATCTCCTGAC	2437
Sbjct	2374	 TGTATTTTTGGTAGAGACGGGGTTTACCATAATTGGCCAGGCTGGTCTCCAACCTCTAAT	2433
Query	2438	CTCAGGTAATCCGCCCGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTG	2497
Sbjct	2434	 CTCAGGTGATCTACCCACCTTGGCCTCCCAAATTGCTGGGATTACAGGCGTGAACCACTG	2493
Query	2498	GGCCCTTCCCTGTCCTG-TGATTTTAAAATAATTATACCAGCAGAAGGACGTCCAGACAC	2556

Score = 3413 bits (1848), Expect = 0.0
Identities = 2120/2249 (94%), Gaps = 27/2249 (1%)
Strand=Plus/Plus

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Query	1022	CTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGG-AAGTAATGGGAGGAGACTA	1080
Sbjct	134255	CTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGGAAGTAATGGGAGGAGACTA	134314
Query	1081	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG	1140
Sbjct	134315	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGTGAG	134374
Query	1141	GTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTCTCTT	1200
Sbjct	134375	GTTGCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGACCTTGGTGGGCGGTCTCTT	134434
Query	1201	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTTCCTGCAGAACCCCCA	1260
Sbjct	134435	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTTCCTGCAGAACCCCCA	134494
Query	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Sbjct	134495	GACCTCCCTCTGCTTCTCAGAGTCTATTCCACACCTTCCAACAGGGTGAAAACGCAACA	134554
Query	1321	GAAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGG-ATGGGGTAGACCTGTGGTCAGAGC	1379
Sbjct	134555	GAAATCCGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGGGGAGACCTGTGGTCAGAGC	134614
Query	1380	CCCCGGGCAGCACAGCCACTGCCG-GTCCTTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	1438
Sbjct	134615	CCCCGGGCAGCACAGCCACTGC-GAGTCCCTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	134673
Query	1439	CTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGC	1498
Sbjct	134674	CTCCATGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGTTCCTCAGGAGCGTCTTCGC	134733
Query	1499	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAGA	1558
Sbjct	134734	CAACAGCCTGGTGTATGGCGCCTCGGACAGGAACGTCTATCACCACCTAAAGGACCTAGA	134793
Query	1559	GGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGA-TCC--AATCCTGGGGC	1615
Sbjct	134794	GGAAGGCATCCAAACGCTGCTGGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCCTGGGGC	134853
Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTTAGCAGTCAGGC	1675
Sbjct	134854	CCCACTGGCTTCCAGGGACCGGGGAGAGAAACACTGCTGCCCTCTTTTTAGTAGTCAGGA	134913
Query	1676	GCTGACCCAAGAGAACTACCGTATTCTTTCATTTCCCCTCGTGAATCCTCCAGGCCTTTC	1735
Sbjct	134914	TCTGACCCAAGAGAACTCATCTTATTCTTTCATTTCCCCTGGCGAATCCTCCAGGCCTTTC	134973
Query	1736	TCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCC	1795
Sbjct	134974	TCTACAGCCTGGAGGGGAGGGAGGAAAATGAATGAATGAGAGAGGGAGTGAACAGTGCGC	135033
Query	1796	AAGCGCTTGGCCTCTCCTTCTTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCC	1855
Sbjct	135034	AAGCCCTTGGCCTCTCCTTCTTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCC	135093
Query	1856	GGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACGATG	1915
Sbjct	135094	GGACTGGGTAGATCTTCAAGCAGACCTACAGCAAGTTTGACACAAACTCGCACAAACGATG	135153

Query	1916	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG	1975
Sbjct	135154	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCG	135213
Query	1976	AGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	2035
Sbjct	135214	AGACATTCTGCGCACCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAACTGC	135273
Query	2036	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGT-CGTGGAAGGTGCTACT	2094
Sbjct	135274	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTTCTGGTTC-TGGAAGGTGCCACT	135332
Query	2095	CCAGTGCCCAACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTGTTGACTAGGTG	2154
Sbjct	135333	CCAGTGCCCAACCAGCCTTGTCCTAATAAAATTAAGTTGCATCATTTTGTCTGACTAGGTG	135392
Query	2155	TCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA	2214
Sbjct	135393	TCCTTCTATAATATTATGGAGTGGAGGGGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA	135451
Query	2215	GACAACCTGTAGGGCCTTCAGGGTCTATTTCGGGAACCAGGCTGGAGTGCAGTGGCA-G-T	2272
Sbjct	135452	GACGACCTGTAGGGCCTGCGGGGCCTATT-GGGAACCAGGCTGGAGCGCAGTGGCACGAT	135510
Query	2273	CTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCG	2332
Sbjct	135511	CGTGGCTCACTACAACCTCCGTCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCG	135570
Query	2333	AATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTGGTAGA	2392
Sbjct	135571	AATAGTTGGGATTCCAGGCATGCACGACCAGGCTCAGCTAATTTTTGTATTTTGGTAGA	135630
Query	2393	GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC	2452
Sbjct	135631	GATGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGATCTCAGGTAATCCTCC	135690
Query	2453	CGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTC-	2511
Sbjct	135691	CGCCTTGGCCTCCCAAATTGCTGGGATTACAGGTAGGAGCCACTGGGCCCTTCCCTGTCT	135750
Query	2512	CTGTGATTTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTG	2571
Sbjct	135751	C-GTGATTTTAAATAATTATACCAGCAGGAGGACGTCCAGACACAGCATGGGCTACCTG	135809
Query	2572	GCCATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTG	2631
Sbjct	135810	GCCGTGCCCAGCCGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCGTTG	135869
Query	2632	GGTCCACTCAGTAGATGCTTGTTGAATTC	2660
Sbjct	135870	GGTCCACTCAGTAGATGCTTGTTGAATTC	135898

Score = 2963 bits (1604), Expect = 0.0
 Identities = 2075/2294 (90%), Gaps = 65/2294 (2%)
 Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCCCT	60
Sbjct	141098	GAATTCAGGAGTGAATGGTGCTCAGAACCCCAATCTATTGGCTGTGC-TTGGCCCCCT	141156

Query	1825	ACTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTAC	1884
Sbjct	142935	ACTTTGCAGAGGCTGGAAGATGGCAGCCCCAGACTAGGCAGACCCTCAAGCAGACCTAT	142994
Query	1885	AGCAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCTC	1944
Sbjct	142995	AACAAGTTTGACACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCTGCGC	143054
Query	1945	TACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGC	2004
Sbjct	143055	CACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGC	143114
Query	2005	TCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCCA	2064
Sbjct	143115	TCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCCGCGTGGCATCC-TGTGACCCCTCCCCA	143173
Query	2065	GTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCACCAGCCTTGTCTAATAAAAA	2124
Sbjct	143174	GTGCCTCTCCTGGCCCCGGAAGGTGCCACTCCAGTGCCACCAGCCTTGTCTAATAAAAA	143233
Query	2125	TTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAG-GCG	2183
Sbjct	143234	TAAAGTTGTATCATTTTGTCTGACCAGGTGTCCTTCTATAATATTATGGGGTGGAAAGTG	143293
Query	2184	GGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATT	2243
Sbjct	143294	G-TGGTATGGAGCAAGGGGC-AGGT-GGGAAGACGACCTGGAGGGCCTTCAGGGTCTATT	143350
Query	2244	CGGGAACCAGGCTG 2257	
Sbjct	143351	-GGGAACCTAGGCTG 143363	

Score = 2817 bits (1525), Expect = 0.0
 Identities = 2052/2297 (89%), Gaps = 74/2297 (3%)
 Strand=Plus/Plus

Query	1	GAATTCAGCACTGAATC-ATGCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCC	59
Sbjct	156338	GAATTCAGGAGTGAA-CGGTGCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCC	156395
Query	60	TTTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAA	119
Sbjct	156396	TTTTCCCTACACACACATTCTGTCTGGTGGGCGGAGGTTCAACATGCGGGGAGGAGGAAA	156455
Query	120	GGAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGAC	179
Sbjct	156456	GGAACAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGAC	156514
Query	180	ATCCTTCTCCGCGTTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACC	239
Sbjct	156515	ATCCTTCCCCGCGTTTTCAGGTTGGCCATCATGGCCTGCTGCCAGAGGGCACCCACCTGACC	156574
Query	240	CTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACA	299
Sbjct	156575	CTTAAAGAGAGAACGAGTTGGGTGCTGTCTCTGGCTGACACTCTGTGCACAACCCTCACA	156634
Query	300	ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT	359

Sbjct	156635	ACGCTGCTGACGGTGGGAAGGGAAAGATGACGAGCCAGGGGGCATGATCCCAGCATGTGT	156694
Query	360	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACAT	419
Sbjct	156695	GGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	156754
Query	420	GCAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCAGG-TATAAAAAGGGCCC	478
Sbjct	156755	ACACAGAAACAGGTGGGGTCAAGCAGGGAGAGAGAAGGGGGCCAGGTATAAAAAGGGCCC	156814
Query	479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCCAAC-TCCCCGAACCACTCAGGGTCTCTGTG	537
Sbjct	156815	GCAAGAGACCAGCTCCAGGATCCCAAGGCCCAACATACCC-AACCACTCACGGTCTCTGTG	156873
Query	538	GACAGCTCAC-TAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTTGG-CACAA	595
Sbjct	156874	GACAGCTCACCTAGCTGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCGTTGGGCAAAA	156933
Query	596	TGTGTCCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCTCAGGTT	655
Sbjct	156934	TGTGTCCGGAGGGGAGAGGCGGCGCCCTGTAGATGGGACGGGGGCACTAACCCTCAGATT	156993
Query	656	TGGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCAG-TATTTGGCCAATCTCTGAAT	714
Sbjct	156994	TGGGGATTCTGAATGTGAA-TATCGCCATCGAAGCCAGATATTTGGCCAGTCTCTGAAT	157052
Query	715	GTTTCCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAAAAAACCAGCTCCTGG	774
Sbjct	157053	GTTTCCTGGTCCCTGGAGG-GAC-G-GAGAGAGAGA-A-AAATCAAG--C--AGCTCCTGG	157103
Query	775	AACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTC-TGTTGCC-TCCGTTTCTCC	832
Sbjct	157104	AACAGGGGGAGTGCTGGTCTCCTGCTCTCCGGCTCCCTCCT-TTGCCCTCCGTTTCTCC	157162
Query	833	CCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAA	892
Sbjct	157163	CCAGGCTCCCGGATGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAC	157222
Query	893	GAGGGCAG-TGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCG	951
Sbjct	157223	CAGG-CTGGTGCCGTCCAAACCGTTCCGTTAGCCAGGCTTTTTGACCATGCTATGCTTCA	157281
Query	952	CGCCCGTCGC-CTGTACCAGCTGGC-ATATGACACCTATCAGGAGTTTGTAAAGCTCTTGG	1009
Sbjct	157282	AGCCCATCACGC-GCACCAACTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGCTCTTGG	157339
Query	1010	GTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGA-AGTAAT	1068
Sbjct	157340	GGAATGGGTGCGGGTCAGGGGTGGCAAGAAGGGGTGACTTTCCCCCACTGGGGTAGTAAT	157399
Query	1069	GGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCAT	1128
Sbjct	157400	GGGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGGAGCGAAAATGCAGGCAGATGAGCAT	157459
Query	1129	ACGCTGAGTGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGA---C--	1183
Sbjct	157460	AGGCTGAGCCAGGTTCCCAGAAACGTAACAATGGGAGCTGGTCTCCAGCATAGAAAGCAG	157519
Query	1184	C--T--T----GGTGGGCGGT----C-C-TTCTCCTAGGAAGAAGCCTATAT-CCTGAAG	1228

Sbjct	157520	CGGTCCTTCATGGGGGGGGGGGGGGCGCATTCTCCTAGGAAGAAGCCTATATTCCA-AAG	157578
Query	1229	GAGCAGAAGTATTTCATTCTGCA-GAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTAT	1287
Sbjct	157579	GAACAGAAGCATTTCATTCTGCATGA-CTCCCAGACCTCC-T--GCTCCTCAGACTCTAT	157634
Query	1288	TCCAACACCTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGGATGCCTTCTCCC	1347
Sbjct	157635	TCCAACACCCTCCAACATGGAGGAAACACAGCAGAAATCCGTGAGTGGATGCCTTCTCCC	157694
Query	1348	CAGGTGGG-ATGGGGTAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTC	1406
Sbjct	157695	CAGGCGGGGATGGGGGAGACCTGTGGTCAGAGCCCCGCGCAGCACAGCCACTGTCCGGTC	157754
Query	1407	CTTCCCCTGCAGAAC-CTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCT	1465
Sbjct	157755	CTTCCCCTGTAGAACTC-AGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCGTGGCT	157813
Query	1466	GGAGCCCGTGCGCTCCTCAGGAGCGTCTTCGCCAAC-AGCCTGGTGTATGGCGCCTCGG	1524
Sbjct	157814	GGAGCCCGTGCGGTTCTCAGGAGTATCTTCGCCAACGA-CCTGGTGTATGACACCTCGG	157872
Query	1525	ACAGCAACGTCTATCG-CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGG	1583
Sbjct	157873	ACAGCAATGACTAT-GACCTCTAAAGGACCTAGAAGAAGGCATCCAAACGCTGATGGGG	157931
Query	1584	GTGAGGGTGGCACCAGGA-TCC--AATCCTGGGGCCCCACTGGCTTCCAGGGACTGGGG-	1639
Sbjct	157932	GTGAGGGCGGTGCCAGGGTCCCCAATCCTGGAACCCCACTGGCTTGGAGGG-CTGGGGG	157990
Query	1640	AGAGAAACACTGCTGCCCTCTTTTTCAGTCAGGCGCTGACCCAAGAGAACTCACCGTA	1699
Sbjct	157991	AGAGAAACACTGCTGCCCTCTTTCTAGTCAGTCAGGCGCTGACCCAAGAGAACTCACCTTA	158050
Query	1700	TTCTTCATTTCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGG	1759
Sbjct	158051	TTCTTCATTTCCCTGGCGAATCCTCCAGGCCTTTCTCTACACCCTGAACGGGAGGGAGG	158110
Query	1760	AAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTT	1819
Sbjct	158111	AAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTT	158170
Query	1820	CCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGT	1879
Sbjct	158171	CCTTCACTTTGCAGAGGCTGGAAGACGGCAGCCCCAGACTGGGCAGACCCTCAAGCAGA	158230
Query	1880	CCTACAGCAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGC	1939
Sbjct	158231	CCTACAGCAAGTTTGACACAAACTCGCACAAACATGACGCACTGCTCAAGAACTACGGGC	158290
Query	1940	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGT	1999
Sbjct	158291	TGCTCCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGT	158350
Query	2000	GCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCT	2059
Sbjct	158351	GCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCGCGTGGCATCC-TGTGACCCCT	158409
Query	2060	CCCCAGTGCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTCTAA	2119

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Sbjct  158410  CCCCAGTGCCTTTTCCTGGCCCCGGAAGGTGCCACTCCAGTGCCCACCAGCCTTGTCTCTAA  158469
Query  2120    TAAAATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGA  2179
          |||||
Sbjct  158470  TAAAATTAAGTTGCATCATTTTCGTCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGA  158529
Query  2180    G-GCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGT  2238
          | || |||||
Sbjct  158530  AAGTGG-TGGTATGGAGCAAGGGGC-AGGT-GGGAAGACGACCTGTAGGACCTTCCGGAT  158586
Query  2239    CTATTCGGGAACCAGGC  2255
          |||| ||||| ||||
Sbjct  158587  GTATT-GGGAAGTAGGC  158602

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Score = 243 bits (131), Expect = 5e-60
 Identities = 218/259 (84%), Gaps = 10/259 (3%)
 Strand=Plus/Plus

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Query  2250    CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA  2307
          |||||
Sbjct  32226    CCAGGCTGGAGTGCAGTGTAGAGCAATCTTGGCTCACTGCGACCTCCGCCTCCTGGGTTCAA  32285
Query  2308    GCGATTCTCCTGCCTCAGTCT-CCCGAATAGTTGCGATTCCAGG--CATGCAAGACCA-G  2363
          |||||
Sbjct  32286    GCGATTCTCCTACTTCAG-CTTCCCAGTAGCTGGGATTACAGGTGCGTGCCA--CCACG  32342
Query  2364    GCTCAGCTAATTTTTGTATTTTTTGGTAGAGACGGGGTTTTACCATATTGGCCAGTCTGGT  2423
          | |||||
Sbjct  32343    GG-CAGCTAATTTTTGTATTTTTATTAGAGACGGGGTTTTACCATGTTGGCCAGGCTGGT  32401
Query  2424    CTCCATCTCCTGACCTCAGGTAATCCGCCCCGCTCGGCCTCCCAAATTGCTGGGATTACA  2483
          ||| | |||| | ||||| || |||| |||||
Sbjct  32402    CTCAAACCTCCCAATCTCAGGTGATCTGCCCACCTCGGCCTCCCAAAGTGCTGGGATTATA  32461
Query  2484    GGTATGAGCCACTGGGCCC  2502
          || |||||
Sbjct  32462    GGCGTGAGCCACTGTGCCC  32480

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Score = 156 bits (84), Expect = 6e-34
 Identities = 155/189 (82%), Gaps = 5/189 (2%)
 Strand=Plus/Plus

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Query  2276    GGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCC-GAA  2334
          |||| | ||| |||||
Sbjct  26789    GGCTCACCGCACCCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAG-CTTCCTGAG  26847
Query  2335    TAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAG-CTAATTTTTGTATTTTTGGTAGAG  2393
          ||| || |||| ||||| |||| | | | ||||| ||||| |||||
Sbjct  26848    TAGCTGGGATTACAGGCATGCGCCACCACAC-CTGGCTAATTTT-GTATTTTGTAGTAGAG  26905
Query  2394    ACGGGGTTTTACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCC  2453
          || ||||| |||| |||| ||| ||| ||| | |||| ||||| ||||| |||
Sbjct  26906    ACAGGGTTTCTCCATGTTGGTCAGGCTGATCTTGAACCTCCCGACCTCAGGTAATCCACCC  26965
Query  2454    GCCTCGGCC  2462
          | |||||
Sbjct  26966    ACTTCGGCC  26974

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Score = 143 bits (77), Expect = 5e-30
Identities = 206/265 (77%), Gaps = 21/265 (7%)
Strand=Plus/Minus

Query	2250	CCAGGCTGGAGTGCAGTGGC-AG-TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA	2307
Sbjct	99767	CCAGGCTGCAGTGCAGTGGCGCATCTCGGCTCACTGAAACCTCTGCCTCCCGGGTTCAT	99708
Query	2308	GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TG-CA--A-GAC	2360
Sbjct	99707	CCCATTCCTCCTGCCTCAGCCTCCC-AAGTGGCTGGGACTACAGGCACCTGCCACCACAAC	99649
Query	2361	CAGGCTCA----GCTAAT-T-T-T-TGTATTTTGGTAGAGACGGGGTTTCACCATATTG	2412
Sbjct	99648	CA-ACTAATTTTTTTTGTGTGTGTGTGTATTTTGGTAGAGACGGGGTTTCACCGTGTTA	99590
Query	2413	GCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCCCTCGGCCTCCCAAATTG	2472
Sbjct	99589	GCCAGGATGGTCTCAATCTCCTGACCTCATG-A-TCCGCCTGCCTTGGACTCCAGAGTG	99532
Query	2473	CTGGGATTACAGGTATGAGCCACTG	2497
Sbjct	99531	CTGGGATTACAGGCGTGAGCCACTG	99507

>emb|CT954302.6| N.leucogenys DNA sequence from clone CH271-262E11, complete sequence
Length=195471

Score = 3402 bits (1842), Expect = 0.0
Identities = 2117/2248 (94%), Gaps = 25/2248 (1%)
Strand=Plus/Minus

Query	432	GTGAGGAGAAGCAGCGAGAGAGAAGGGGCCA-GGTATAAAAAGGGCCCAACAAGAGACCAG 	490
Sbjct	74925	GTGGGGAGAAGCAGCGAGAGAGAAGGGGCCAGGGCATAAAAACGGCCCAACAAGAGACCAG	74866
Query	491	CTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCTGTGGACAGCTCA-CTA 	549
Sbjct	74865	CTCCAGGATCCCAAGGCCCAACTCCCCAAACCACTCAGGGTCTGTGGACAGCTCACCTA	74806
Query	550	GCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTT-GGCACAATGTGTCTGAGGG 	608
Sbjct	74805	GCTGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTTGGGCGCAATGCGTCCAGAGGA	74746
Query	609	GAGAGGCGGCGTCTCTGTAGATGGGACGGGGGCACTAACCTCAGGTTTGGGGCTTATGAA 	668
Sbjct	74745	GAGAGGCGGCGCCCTGTAGATGGGACGGGCACACTAAACCTCAGGTTTGGGGCGTCTGAA	74686
Query	669	TGTTAGCTATCGCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTCTGGTCCCTG 	728
Sbjct	74685	TGTTAG-TATCTCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTCTGGTCCCTG	74627
Query	729	GA-GGAGGCAGAGAGAGAGAGAGAGAG- - - - AAAAAAAAAAACCCAGCTCCTGGAACAGGGAG 	783
Sbjct	74626	GAGGGAGGTTAGAGAGAGAGAGAGAGAGAGAAAAAAAAAAAAAACCCAGCCCCAGGAGCAGGGAG	74567
Query	784	AGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTT-GCCTCCGTTTCTCCCCAGGCTCCC 	842
Sbjct	74566	AGCGCTGGACTCTTGCTCTCCAGCTCCCTCTGTTACCTCCGTTTCTCCCCAGGCTCCC	74507

Query	843	GGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCTGGCTTCAAGAGGGCAGTG	902
Sbjct	74506	GGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGAGGGCAGTG	74447
Query	903	CCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAACGCTATGCTCCGCGCCCGTCGCC	962
Sbjct	74446	CCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAATGCTATGCTCCGCGCCCATCGCC	74387
Query	963	TGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAAGCTC-TTGGGTAATGGGTGCG	1021
Sbjct	74386	TGGACCAGCTGGCATTGTGACACCTACCAGGAGCTTGTAAAGCTCTTTGGG-AATGGGTACG	74328
Query	1022	CTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAATGGGAGGAGACTA	1080
Sbjct	74327	CTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGGAAGTAATGGGAGGAGACTA	74268
Query	1081	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGCAGATGAGCATACGCTGAGTGAG	1140
Sbjct	74267	AGGAGCTCAGGGTTGTTTTCTGAAGTGAAATGCAGGCAGATGAGCATACGCTGAGTGAG	74208
Query	1141	GTTCCCAAGAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGTCTCTT	1200
Sbjct	74207	GTTGCCAAGAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGACCTTGGTGGGCGAGTCCTT	74148
Query	1201	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAACCCCCA	1260
Sbjct	74147	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCCCGCAGAACCCCCA	74088
Query	1261	GACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Sbjct	74087	GACCTCCCTCTGCTTCTCAGAGTCTATTCCCACACCTTCCAACAGGGTGAAAACGCAACA	74028
Query	1321	GAAATCTGTGAGTGGATGCCTTCTCCCCAGGT-GGGATGGGGTAGACCTGTGGTCAGAGC	1379
Sbjct	74027	GAAATCCGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGGGGAGACCTGTGGTCAGAGC	73968
Query	1380	CCCCGGGCAGCACAGCCACTGCCG-GTCCTTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	1438
Sbjct	73967	CCCCGGGCAGCACAGCCACTG-CGAGTCCCTCCCCTGCAGAACCTAGAGCTGCTCCGCAT	73909
Query	1439	CTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGC	1498
Sbjct	73908	CTCCATGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGC	73849
Query	1499	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCTAGA	1558
Sbjct	73848	CAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCACCACCTAAAGGACCTAGA	73789
Query	1559	GGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCA-GGAT--CCAATCCTGGGGC	1615
Sbjct	73788	GGAAGGCATCCAAACGCTGCTGGGGGTGAGGGTGGCGCCAGGGGTCCCCAATCCTGGGGC	73729
Query	1616	CCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCAGGC	1675
Sbjct	73728	CCCACTGGCTTCCAGGGACCGGGAGAGAAACACTGCTGCCCTCTTTTAGTAGTCAGGA	73669
Query	1676	GCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCTTTC	1735
Sbjct	73668	TCTGACCCAAGAGAACTCATCTTATTCTTCATTTCCCCTGGCGAATCCTCCAGGCCTTTC	73609

Query	1736	TCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCC	1795
Sbjct	73608	TCTACAGCCTGGAGGGGAGGGAGGAAAATGAATGAATGAGAGAGGGAGTGAACAGTGCGG	73549
Query	1796	AAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCC	1855
Sbjct	73548	AAGCCCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCCCCC	73489
Query	1856	GGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACGATG	1915
Sbjct	73488	GGACTGGGTAGATCTTCAAGCAGACCTACAGCAAGTTTGACACAAACTCGCACAAACGATG	73429
Query	1916	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCTG	1975
Sbjct	73428	ACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCTG	73369
Query	1976	AGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGC	2035
Sbjct	73368	AGACATTCTGCGCACCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAACTGC	73309
Query	2036	CCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGG-TCGTGGAAGGTGCTACT	2094
Sbjct	73308	CCTGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTTCTGGTTC-TGGAAGGTGCCACT	73250
Query	2095	CCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTTACTAGGTG	2154
Sbjct	73249	CCAGTGCCCACCAGCCTTGTCTTAATAAAATTAAGTTGCATCATTTTGTCTTACTAGGTG	73190
Query	2155	TCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAA	2214
Sbjct	73189	TCCTTCTATAATATTATGGAGTGGAGGGGGGTGGTATGGAGCAAGGGGC-AGGTTGGGAA	73131
Query	2215	GACAACCTGTAGGGCCTTCAGGGTCTATTGCGGAACCAGGCTGGAGTGCAGTGGCA-G-T	2272
Sbjct	73130	GACGACCTGTAGGGCCTGCGGGGTCTATT-GGGAACCAGGCTGGAGCGCAGTGGCACGAT	73072
Query	2273	CTTGGCTCGCTGCAATCTCCGCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCCCG	2332
Sbjct	73071	CGTGGCTCACTACAACCTCTGTCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCTG	73012
Query	2333	AATAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAGCTAATTTTTGTATTTTTGGTAGA	2392
Sbjct	73011	AATAGTTGGGATTCCAGGCATGCACGACCAGGCTCAGCTAATTTTTGTATTTTTGGTAGA	72952
Query	2393	GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCC	2452
Sbjct	72951	GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGATCTCAGGTAATCCTCC	72892
Query	2453	CGCCTCGGCCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCC	2512
Sbjct	72891	CGCCTTGGCCTCCCAAATTGCTGGGATTACAGGTAGGAGCCACTGGGCCCTTCCCTGTCT	72832
Query	2513	TGTGATTTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGG	2572
Sbjct	72831	TGTGATTTTAAACATAATTATACCAGCAGGAGGACGTCCAGACACAGCATGGGCTACCTGG	72772
Query	2573	CCATGCCCAGCCAGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTGG	2632
Sbjct	72771	CCATGCCCAGCTGGTTGGACATTTGAGTTGTTTGCTTGGCACTGTCCTCTCATGCATTGG	72712

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Query   2633   GTCCACTCAGTAGATGCTTGTGAATTC   2660
          |||
Sbjct   72711  GTCCACTCAGTAGATGCTTGTGAATTC   72684

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Score = 2913 bits (1577), Expect = 0.0
 Identities = 2067/2295 (90%), Gaps = 67/2295 (2%)
 Strand=Plus/Minus

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Query   1      GAATTCAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTTGGCCCT 60
          |||
Sbjct   67457  GAATTCAGGAGTGAATGGTGTCTAGAACCCCAATCTATTGGCTGTGC-TTGGCCCT 67399

Query   61      TTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAAG 120
          |||
Sbjct   67398  TTTCCCAACACACACATTCTGTCTGGTGGGCGGAGGTTAAACATGCGGGGAGGAGGAAAG 67339

Query   121     GAATAGGATAGAGAGTGGGATGGGGTCCGTAGGGGTCTCAAGGACTGGCCTATCCTGACA 180
          |||
Sbjct   67338  GATTAGGATAGAGAGTGGGATGGGGTCCGTAGGGGTCTCAAGGACTGG-CTATCCTGACA 67280

Query   181     TCCTTCTCCGCGTTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC 240
          |||
Sbjct   67279  TCCTTCCCCGCGTTTCAGGTTGGCCACCATGACCTGCTGCCAGAGGGCACCCACCTGA-CC 67221

Query   241     TTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACAA 300
          |||
Sbjct   67220  TTAAAGAGCGGACAAGTTGGGTGGTGTCTCTGGCTGACACTCTGTGCACAACCCTCACAA 67161

Query   301     CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG 360
          |||
Sbjct   67160  CGCTGCTCACGGTGGGAAGGGAAAGATGACGAGCCAGGAGGCATGATCCCAGCATGTGTG 67101

Query   361     GGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATG 420
          |||
Sbjct   67100  GGAGGAGCTTCTGAATTATCCATTAGCACAAAGCCCATCAGTGGCCCCAGGCCTAAACGTG 67041

Query   421     CAGAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGGCCA-GGTATAAAAAGGGCCCA 479
          |||
Sbjct   67040  CAGAGAAACAGGTGGGGAGAAGCAGCGAGAGAGAAGGGGGCCAGGGTATAAAAAGGGCCCG 66981

Query   480     CAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGA 539
          |||
Sbjct   66980  CAAGAGACCAGCTCCAGGATCCCAAGGCCCAACTCCCCAAACCACTCAGGGTCCTGTGGA 66921

Query   540     CAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTT-GGCACAATG 597
          |||
Sbjct   66920  CAGCTCACCTAGCCGCAAAGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTTGGGCACAGTG 66861

Query   598     TGTCTGAGGGGAGAGGCGGCGT-CCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT 656
          |||
Sbjct   66860  TGTCCCAAGGGGAGAAGCGGC-TCCCTGTAGATGGGACGGGGGCACTAACCTCAGGTTT 66802

Query   657     GGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAG-TATTTGGCCAATCTCTGAATG 715
          |||
Sbjct   66801  GGGGCTCCTGAATGTGA-ATATCGCCATCGAAGTCCAGATATTTGGCCAATCTCTGAATG 66743

Query   716     TTCCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 775
          |||

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Sbjct	66742	TTCCTGGTCCC---CGGAGG--GA-CG-GAGAGAGAGAAAAAACAA-GCAGCTCCTGGA	66691
Query	776	ACAGGGAGAGCGCTGGCCTCTTGGCTCTCCAGCTCCCT-CTGTTG-CCTCCGGTTTCTCCC	833
Sbjct	66690	ACAGGGAGAGTGTGGCCTCCTGGTCTCCGGCTCCCTCCT-TTGCCCTCCGGTTTCTCCC	66632
Query	834	CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAG	893
Sbjct	66631	CAGGCTCCCAGATGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCACC	66572
Query	894	AGGGC-AGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACA-ACG-CTATGCTCC	950
Sbjct	66571	A-GGCTGGTGCCGTCCAAACCGTTCCCTTAGCCAGGCTTTTTGA-AGA-GACTATGTTCC	66515
Query	951	GCGCCCGTCGC-CTGTACCAGCTGG-CATATGACACCTATCAGGAGTTTGTAAAGCTCTTG	1008
Sbjct	66514	AAGCCCATCGCGC-GCACCAGCTGGCCAT-TGACACCTACCAGGAGTTTGTAAAGCTCTTG	66457
Query	1009	GGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCT-GGGAAGTAA	1067
Sbjct	66456	GGGAATGGGTGCGGGTCAGGGGTGGCAAGAACGGGTGACTTTCCCCCACTGGGGAAGTAA	66397
Query	1068	TGGGAGGAGACTAAGGAGCTCAGGGTTGTTT-TCTGAAGTGAAAATGCAGGCAGATGAGC	1126
Sbjct	66396	TGGGAGGAGACTAAGGAGCTCAGGGTT-TTTATCTGGAGCGAAAATGCAGGCAGATGAGC	66338
Query	1127	ATACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCAT----AG-	1181
Sbjct	66337	ATAGGCTGAGCCAGGTTCCAGAAAAGTAACAATGAGAGCTGGTCTCCAGCATAGAAAGC	66278
Query	1182	A-----C--CTT--GG-TGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAG	1231
Sbjct	66277	AGCTTTCTTCTTGGGGCGGGGGGTCTTCTCCTAGGAAGAAGCCTATATCCCAAAGGAC	66218
Query	1232	CAGAAGTATTCAATTCCTGCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCA	1291
Sbjct	66217	CAGAAGTATTCAATTCCTGCATAACCCCCAGACTTCTTCTGCTTCTCAGACTCTATTCCA	66158
Query	1292	ACACCTTCCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGATGCCTTCTCCCCAGG	1351
Sbjct	66157	ACACCCTCCAACAGGAAGGAAACACAGCAGAAATCCGTGAGTGATGCCTTCTCCCCAGG	66098
Query	1352	-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCTTTC	1410
Sbjct	66097	CGGGGATGGGGGAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGTCGGTCTTTC	66038
Query	1411	CCCTGCAGAACCT-AGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAG	1469
Sbjct	66037	CCCTGCAGAA-CTCAGAGCTGCTCCGCATCTCCCTGCGGCTCATGGAGTCGTGGCTGGAG	65979
Query	1470	CCCGTGCAGCTCCTCAGGAGCGTCTTCGCCAACAG-CCTGGTGTATGGCGCCTCGGACAG	1528
Sbjct	65978	CCCGTGCGGTTCCTCAGGAGTATCTTACCAAC-GACCTGGTGTATGACACCTCGGACAG	65920
Query	1529	CAACGTCTATCG-CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGA	1587
Sbjct	65919	CGATGACTAT-GACCTCCTAAAGGACCTAGAAGAAGGCATCCAAACGCTGATGGGGGTGA	65861
Query	1588	GGGTGGCACCA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACT-GGGGAGAG	1643

Sbjct	65860	GGGTGGCCCCAGGGGTCCCCAATCCTGGGGCCCCACTGGCTTCAAGGG-CTGGGGGAGAG	65802
Query	1644	AAACACTGCTGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCT 	1703
Sbjct	65801	AAACACTGCTGCCCTCTTTCTAGCAGTCAGGCACTGACCCAAGAGAACTCACCTTATTCT	65742
Query	1704	TCATTTCCCCTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAA 	1763
Sbjct	65741	TCATTTCCCCTGGCGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAAA	65682
Query	1764	TGGATGAATGAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTT 	1823
Sbjct	65681	TGGATGAATGAGAGAGCGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTT	65622
Query	1824	CACTTTGCAGAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTA 	1883
Sbjct	65621	CACTTTGCAGAGGCTGGAAGACGGCAGCCCCAGACTGGGCAGACCCTCAAGCAGACCTA	65562
Query	1884	CAGCAAGTTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGCTGCT 	1943
Sbjct	65561	TAACAAGTTTGACACAAACTCGCACAAACATAACGCACTGCTCAAGAACTACGGGCTGCG	65502
Query	1944	CTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG 	2003
Sbjct	65501	CCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG	65442
Query	2004	CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTCCCC 	2063
Sbjct	65441	CTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCCGCGTGGCATCC-TGTGACCCCTCCCC	65383
Query	2064	AGTGCCTCTCCTGGTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAATAAA 	2123
Sbjct	65382	AGTGCCTCTCCTGGCCCCGGAAGGTGCCACTCCAGTGCCCACCAGTCTTGTCTTAATAAA	65323
Query	2124	ATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAG-GC 	2182
Sbjct	65322	ATAAAGTTGTATCATTTTGTCTGACCAGGTGTCCTTCTATAATATTATGGGGTGGAAAGT	65263
Query	2183	GGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTAT 	2242
Sbjct	65262	GG-TGGTATGGAGCAAGGGGC-AGGT-GGGAAGACGACCTGGAGGGCCTTCAGGGTCTAT	65206
Query	2243	TCGGAACCAAGGCTG 2257 	
Sbjct	65205	T-GGGAAGTGGGCTG 65192	

Score = 2832 bits (1533), Expect = 0.0
Identities = 2054/2296 (89%), Gaps = 73/2296 (3%)
Strand=Plus/Minus

Query	1	GAATTCAGCACTGAATC-ATGCCCAGAACCCCCGCAATCTATTGGCTGTGCTTTGGCCCC 	59
Sbjct	52167	GAATTCAGGAGTGAA-CGGTGTCTCAGAACCCCCACAATCTATTGGCTGTGC-TTGGCCCC	52110
Query	60	TTTTCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAA 	119
Sbjct	52109	TTTTCCCTACACACACATTCTGTCTGGTGGGCGGAGGTTCAACATGCGGGGAGGAGGAAA	52050
Query	120	GGAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGTCTCAAGGACTGGCCTATCCTGAC	179

Sbjct	50274	 CTACAGCAAGTTTGCACAAACTCGCACAAACCATGACGCACTGCTCAAGAACTACGGGCT	50215
Query	1941	GCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAAGTG	2000
Sbjct	50214	 GCTCCACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCCTGCGCATCGTGCAAGTG	50155
Query	2001	CCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCCGGGTGGCATCCCTGTGACCCCTC	2060
Sbjct	50154	 CCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGGTGCCCCGCGTGGCATCC-TGTGACCCCTC	50096
Query	2061	CCCAGTGCCCTCTCCTGGTTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTTAAT	2120
Sbjct	50095	 CCCAGTGCCCTTTCCTGGCCCCGGAAGGTGCCACTCCAGTGCCCACCAGCCTTGTCTTAAT	50036
Query	2121	AAAATTAAGTTGCATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAG	2180
Sbjct	50035	 AAAATTAAGTTGCATCATTTTCGTCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGAA	49976
Query	2181	-GCGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTTC	2239
Sbjct	49975	 AGTGG-TGGTATGGAGCAAGGGGC-AGGT-GGGAAGACGACCTGTAGGACCTTCCGGATG	49919
Query	2240	TATTCGGAACAGGC 2255	
Sbjct	49918	 TATT-GGGAACAGGC 49904	

Score = 243 bits (131), Expect = 5e-60
 Identities = 218/259 (84%), Gaps = 10/259 (3%)
 Strand=Plus/Minus

Query	2250	CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA	2307
Sbjct	176382	 CCAGGCTGGAGTGCAGTGTAGAGCAATCTTGGCTCACTGCGACCTCCGCCTCCTGGGTTCAA	176323
Query	2308	GCGATTCTCCTGCCTCAGTCT-CCCGAATAGTTGCGATTCCAGG--CATGCAAGACCA-G	2363
Sbjct	176322	 GCGATTCTCCTACTTCAG-CTTCCCGAGTAGCTGGGATTACAGGTGCGTGCCA--CCACG	176266
Query	2364	GCTCAGCTAATTTTTGTATTTTTGGTAGAGACGGGGTTTACCATATTGGCCAGTCTGGT	2423
Sbjct	176265	 GG-CAGCTAATTTTTGTATTTTTATTAGAGACGGGGTTTACCATGTTGGCCAGGCTGGT	176207
Query	2424	CTCCATCTCCTGACCTCAGGTAATCCGCCCGCCTCGGCCTCCCAAATTGCTGGGATTACA	2483
Sbjct	176206	 CTCAAATCCCAATCTCAGGTGATCTGCCACCTCGGCCTCCCAAAGTGTGGGATTATA	176147
Query	2484	GGTATGAGCCACTGGGCCC 2502	
Sbjct	176146	 GGCGTGAGCCACTGTGCCC 176128	

Score = 226 bits (122), Expect = 5e-55
 Identities = 214/258 (82%), Gaps = 8/258 (3%)
 Strand=Plus/Plus

Query	2250	CCAGGCTGGAGTGCAGT-G-GCAGTCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA	2307
Sbjct	32543	 CCAGGCTGGAGTGCAGTCGCACAATCTCGGCTAACTGCAACCTCCGCCTCCTGGGTTCAA	32602

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Query   2308   GCGATTCTCCTGCCTCAGTCTCCCGAATAGTTGCGATTCCAGGCATGCAAGACCAGGC-T   2366
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   32603   GCGATTCTCCGGCCTCAGCCTCCCGAGTAGCTGGGATTATAGGCACCCACCACCATGCCT   32662

Query   2367   CAGCTAATTTTTGTATTTTTG--GTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTC   2424
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   32663   GA-CTAATTTT-GTATTTTTTTAGTAGAGATGGGGTTTCATGATGTTGGCCAGGCTGGTC   32720

Query   2425   TCCATCTCCTGACCTCAGGTAATCCGCCC GCCTCGGCCTCCCAAATTGCTGGGATTACAG   2484
          | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   32721   TGAAACTCCT-ACCTCAGGTGATCCACCCACCTCAGCCTCCTAAAGTGCTGGGATTACAG   32779

Query   2485   GTATGAGCCACTGGGCCC   2502
          ||||| ||||| | ||||
Sbjct   32780   GTATGAGCCACCGTGCCC   32797

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Score = 217 bits (117), Expect = 3e-52
 Identities = 208/251 (82%), Gaps = 9/251 (3%)
 Strand=Plus/Minus

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Query   2250   CCAGGCTGGAGTGCAGTGGC-AG-TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA   2307
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   21738   CCAGGCTGGAGTGCAGTGGCGCGATCCCGGCTCACTGCAACCTCTGCCTCCTGGGTTCAA   21679

Query   2308   GCGATTCTCCTGCCTCAGTCTCCCGAATAGTT-GCGATTCCAGGCA-TGCAAGACCAGGC   2365
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   21678   GCGATTCTCCTGCCTCAGCCTCCCGAGTAAGTAG-GACTGCAGG-AGTGTGCCACCACGC   21621

Query   2366   TCAGCTAATTTTT-GTATTTTTGGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTC   2424
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   21620   CCAGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTAGCCAGGATGGTC   21561

Query   2425   TCCATCTCCTGACCTCAGGTAATCCGCCC GCCTCGGCCTCCCAAATTGCTGGGATTACAG   2484
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   21560   TCAATCTCCTGACCTT-G-TGATCCACCCACCTTGGCCTCCCAAAGTGCTGGGATTACAG   21503

Query   2485   GTATGAGCCAC   2495
          | ||||| ||||
Sbjct   21502   GCGTGAGCCAC   21492

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Score = 156 bits (84), Expect = 6e-34
 Identities = 155/189 (82%), Gaps = 5/189 (2%)
 Strand=Plus/Minus

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Query   2276   GGCTCGCTGCAATCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCC-GAA   2334
          ||||| | ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   181786   GGCTCACCGCACCCCTCCGCCTCCTGGGTTCAAGCGATTCTCCTGCCTCAG-CTTCTGAG   181728

Query   2335   TAGTTGCGATTCCAGGCATGCAAGACCAGGCTCAG-CTAATTTTTGTATTTTTGGTAGAG   2393
          ||| || |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   181727   TAGCTGGGATTACAGGCATGCGCCACCACAC-CTGGCTAATTTT-GTATTTTTAGTAGAG   181670

Query   2394   ACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCCTGACCTCAGGTAATCCGCCC   2453
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   181669   ACAGGGTTTCTCCATGTTGGTCAGGCTGATCTTGAACCTCCCGACCTCAGGTAATCCACCC   181610

Query   2454   GCCTCGGCC   2462

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Score = 148 bits (80), Expect = 1e-31
Identities = 207/265 (78%), Gaps = 21/265 (7%)
Strand=Plus/Plus

Query	2250	CCAGGCTGGAGTGCAGTGGC-AG-TCTTGGCTCGCTGCAATCTCCGCCTCCTGGGTTCAA 	2307
Sbjct	108830	CCAGGCTGCAGTGCAGTGGCGCATCTCGGCTCACTGAAACCTCTGCCTCCCGGGTTTCAT	108889
Query	2308	GCGATTCTCCTGCCTCAGTCTCCCGAA-TAGTTGCGATTCCAGGCA--TG-CA--A-GAC 	2360
Sbjct	108890	CCCATTCTCCTGCCTCAGCCTCCC-AAGTGGCTGGGACTACAGGCACCTGCCACCACAAC	108948
Query	2361	CAGGCTCA----GCTAAT-T-T-T-TGTAATTTTTGGTAGAGACGGGGTTTTACCATATTG 	2412
Sbjct	108949	CA-ACTAATTTTTTTTTTGTGTGTGTGTATTTTTGGTAGAGACGGGGTTTTACCGTGTTA	109007
Query	2413	GCCAGTCTGGTCTCCAICTCCTGACCTCAGGTAATCCGCCCCGCTCGGCCTCCCAAATTG 	2472
Sbjct	109008	GCCAGGATGGTCTCAATCTCCTGACCTCATG-A-TCCGCCTGCCTTGGCCTCCCAGAGTG	109065
Query	2473	CTGGGATTACAGGTATGAGCCACTG	2497
Sbjct	109066	CTGGGATTACAGGCGTGAGCCACTG	109090

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>gb|EU421712.1| Homo sapiens growth hormone 1 (GH1) gene, complete cds, alternatively spliced
Length=2212
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Score = 3254 bits (1762), Expect = 0.0
Identities = 2084/2235 (93%), Gaps = 39/2235 (1%)
Strand=Plus/Plus

Query	106	CGGGGAGGAGGAAAAGGAATAGGATAGAGAGTGGGATGGGGTTCGGTA-GGGGTCTCAAGGA	164
Sbjct	1	CGGGGAGGAGGAAAAGGGATAGGATAGAGAATGGGATGTGGTTCGGTAGGGGTCTCAAGGA	60
Query	165	CTGGCCTATCCTGACATCCTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAG	224
Sbjct	61	CTGG-CTATCCTGACATCCTTCGCCGCGTGCAGGTTGGCCACCATGGCCTGCTGCCAGAG	119
Query	225	GGCACCACGTGACCCTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTG	284
Sbjct	120	GGCACCACGTGACCCTTAAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACACTCTG	179
Query	285	TGCACAACCCTCACAACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCAT	344
Sbjct	180	TGCACAACCCTCACAACACTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGGCAT	239
Query	345	GATCCCAGCATGTGTGGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGC	404
Sbjct	240	GATCCCAGCATGTGTGGGAGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGC	299
Query	405	CCCAGGCCTAAACATGCAGAGAAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCA-	462
Sbjct	300	CCCATGCATAAATGTACACAGAAACAGGTG-GGGGCAA-CAGTGGGAGAGAAGGGGCCAG	357

Query	463	GGTATAAAAAGGGCCCCACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACC	522
Sbjct	358	GGTATAAAAAGGGCCCCACAAGAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACC	417
Query	523	ACTCAGGGTCCTGTGGACAGCTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAA	581
Sbjct	418	ACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTACAGGTAAGCGCCCCCTAAAA	477
Query	582	TCCCTTT-GGCACAATGTGTCTCTGAGGGGAGAGGCGGCTCTGTAGATGGGACGGGGGC	640
Sbjct	478	TCCCTTTGGGCACAATGTGTCTCTGAGGGGAGAGGCAGCGACCTGTAGATGGGACGGGGGC	537
Query	641	ACTAACCCTCAGGTTTGGGGCTTATGAATGTTAGCTATCGCCATCTAAGCCCAGTATTTG	700
Sbjct	538	ACTAACCCTCAGGTTTGGGGCTTCTGAATGTGAG-TATCGCCATGTAAGCCCAGTATTTG	596
Query	701	GCCAATCTCTGAATGTTTCTGGTCCCTGGAGGAGGCAGAGAGAGAGAGAGAGAGAAAAAAA	760
Sbjct	597	GCCAATCTCAGAAAGCTCCTGGTCCCT---GGA-G--G-GA-TG-GAGAGAG-AAAAACA	646
Query	761	AACCCAGCTCCTGGAACAGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-C	819
Sbjct	647	AA--CAGCTCCTGGAGCAGGGAGAGTGCTGGCCTCTTGCTCTCCGGCTCCCTCTGTTGCC	704
Query	820	CTCCGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCT	879
Sbjct	705	CTCTGGTTTCTCCCCAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCT	764
Query	880	GTCCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAA	939
Sbjct	765	GCCCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTTATCCAGGCTTTTTGACAA	824
Query	940	CGCTATGCTCCGCGCCCGTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGT	999
Sbjct	825	CGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCTTTGACACCTACCAGGAGTTTGT	884
Query	1000	AAGCTCTTGGGTAATGGGTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTG	1059
Sbjct	885	AAGCTCTTGGGGAATGGGTGCGCATCAGGGGTGGCAGGAAGGGGTGACTTTCCCCCGCTG	944
Query	1060	GGAAGTAATG-GGAGGAGACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGC	1118
Sbjct	945	GGAAATAA-GAGGAGGAGACTAAGGAGCTCAGGGTT-TTCCCGAAGCGAAAATGCAGGC	1002
Query	1119	AGATGAGCATACGCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCAGGTCTCCAGCA	1178
Sbjct	1003	AGATGAGCACACGCTGAGTGAGGTTCCCGAGAAAAGTAACAATGGGAGCTGGTCTCCAGCG	1062
Query	1179	TAGACCTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGT	1238
Sbjct	1063	TAGACCTTGGTGGGCGGTCTTCTCCTAGGAAGAAGCCTATATCCCAAAGGAACAGAAGT	1122
Query	1239	ATTCAATTCCTGCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTT	1298
Sbjct	1123	ATTCAATTCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAGTCTATTCCGACACCTT	1182
Query	1299	CCAACAGGGTGAAAACGCAGCAGAAATCTGTGAGTGAGTGCCTTCTCCCCAGG-TGGGAT	1357
Sbjct	1183	CCAACAGGGAGGAAACACAACAGAAATCCGTGAGTGAGTGCCTTCTCCCCAGGCGGGGAT	1242

Query	1358	GGGGTAGACCTGTGGTTCAGAGCCCCCGGGCAGCACAGCCACTGCCGGTCCCTTCCCCTGCA 	1417
Sbjct	1243	GGGGGAGACCTGTAGTCAGAGCCCCCGGGCAGCACAGCCAATGCCCGTCCCTTCCCCTGCA 	1302
Query	1418	GAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCA 	1477
Sbjct	1303	GAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGAGCCCGTGCA 	1362
Query	1478	GCTCCTCAGGAGCGTCTTTCGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTA 	1537
Sbjct	1363	GTTCTCAGGAGTGTCTTTCGCCAACAGCCTGGTGTACGGCGCCTCTGACAGCAACGTCTA 	1422
Query	1538	TCG-CCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCAC 	1596
Sbjct	1423	T-GACCTCCTAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGGGGTGAGGGTGGCGC 	1481
Query	1597	CA-GGAT--CCAATCCTGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGC 	1652
Sbjct	1482	CAGGGGTCCCCAATCCTGGAGCCCCACTGACTTTGAGAG-CTGTGTTAGAGAAACACTGC 	1540
Query	1653	TGCCCTCTTTTTAGCAGTCAGGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCC 	1712
Sbjct	1541	TGCCCTCTTTTTAGCAGACAGGCCCTGACCCAAGAGAACTCACCTTATTCTTCATTTCCC 	1600
Query	1713	CTCGTGAATCCTCCAGGCCTTTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAAT 	1772
Sbjct	1601	CTCGTGAATCCTCCAGGCCTTTCTCTACACCCTGAAGGGGAGGGAGGAAAATGAATGAAT 	1660
Query	1773	GAGAGAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCA 	1832
Sbjct	1661	GAGAAAAGGGAGGGAACAGTACCCAAGCGCTTGGCCTCTCCTTCTCTTCCTTCACTTTGCA 	1720
Query	1833	GAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTT 	1892
Sbjct	1721	GAGGCTGGAAGATGGCAGCCCCCGGACTGGGCAGATCTTCAAGCAGACCTACAGCAAGTT 	1780
Query	1893	TGACACAAAATCGCACACGATGACGCACTGCTCAAGAACTACGGGGCTGCTCTACTGCTT 	1952
Sbjct	1781	CGACACAAACTCACACAACGATGACGCACTACTCAAGAACTACGGGGCTGCTCTACTGCTT 	1840
Query	1953	CAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGA 	2012
Sbjct	1841	CAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGA 	1900
Query	2013	GGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCT 	2072
Sbjct	1901	GGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCT 	1960
Query	2073	CCTGGTCGTGGAAGGTGCTACTCCAGTGCCCACCAGCCTTGTCTAATAAAATTAAGTTG 	2132
Sbjct	1961	CCTGGCCCTGGAAGTTGCCACTCCAGTGCCCACCAGCCTTGTCTAATAAAATTAAGTTG 	2020
Query	2133	CATCATTTTGTGTTGACTAGGTGTCCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATG 	2192
Sbjct	2021	CATCATTTTGTCTGACTAGGTGTCCTTCTATAATATTATGGGGTGGAGGGGGTGGTATG 	2080
Query	2193	GAGCAAGGGGCCAGGTTGGGAAGACAACCTGTAGGGCCTTCAGGGTCTATTCGGGAACCA 	2252
Sbjct	2081	GAGCAAGGGGCAAG-TTGGGAAGACAACCTGTAGGGCCTGCGGGGTCTATT-GGGAACCA 	2138


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Query   2253  GGCTGGAGTGCAGTGGCAG--TCTTGGCTCGCTGCAATCTCCGCC-TCCTGGGTTCAAGC  2309
          |||||
Sbjct   2139  AGCTGGAGTGCAGTGGCACAATCTTGGCTCACTGCAATCTCCGCCCTC-TGGGTTCAAGC  2197

Query   2310  GATTCTCCTGCCTCA  2324
          |||||
Sbjct   2198  GATTCTCCTGCCTCA  2212

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>gb|AF374233.1| Pan troglodytes growth hormone (GH-V) gene, complete cds
Length=1879

Score = 3236 bits (1752), Expect = 0.0
Identities = 1841/1882 (97%), Gaps = 13/1882 (0%)
Strand=Plus/Plus

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Query   183  CTTCTCCGCGTTCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCCTT  242
          |||||
Sbjct    1  CTTCCCCGCGTGCAGGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACCTGCCCCCTT  60

Query   243  AAAGAGAGGACAAGTTGGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCTCACAACG  302
          |||||
Sbjct   61  AAAGAGAGGACAAGTTGGGTGGTATCTCT-GCTGACACTCTGTGCACAACCCTCACAACG  119

Query   303  CTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTGGG  362
          |||||
Sbjct  120  CTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGGCATGATCCCAGCATGTGTGGG  179

Query   363  AGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACATGCA  422
          |||||
Sbjct  180  AGGAGCTTCTAAATTATCCATTAGCACAAAGCCCGTCAGTGGCCCCAGGCCTAAACGTGCA  239

Query   423  GAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAAAGGGCCCACAA  482
          |||||
Sbjct  240  GAGAAACAGGTGAGGAGAAGCAGCGAGAGAGAAGGGGCCAGGTATAAAGAGGGCCCACAA  299

Query   483  GAGACCAGCTCAAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAG  542
          |||||
Sbjct  300  GAGACCAGCTCCAGGATCCCAAGGCCCAACTCCCCGAACCACTCAGGGTCCTGTGGACAG  359

Query   543  CTCA-CTAGCGGCAATGGCTGCAGGTAAGCGCCCCCTAAAATCCCTTT-GGCACAATGTGT  600
          |||||
Sbjct  360  CTCACCTAGCGGCAATGGCTGCAGGTAAGCACCCCTAAAATCCCTTTGGGCACAATGTGT  419

Query   601  CCTGAGGGGAGAGGCGGCGTCCTGTAGATGGGACGGGGGCACTAACCCTCAGGTTTGGGG  660
          |||||
Sbjct  420  CCTGAGGGGAGAGGCGGCGTCCTGTAGATTGGACGGGGGCACTAACCCTCAGGTTTGGGG  479

Query   661  CTTATGAATGTTAGCTATCGCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTTCCT  720
          |||
Sbjct  480  CTTCTGAATGTTAG-TATCGCCATCTAAGCCCAGTATTTGGCCAATCTCTGAATGTTTCCT  538

Query   721  GGTCCCTGGA-GGAGGCAGAGAGAGAGAGAG--AGAAAAAAAAAACCCAGCTCCTGGAAC  777
          |||||
Sbjct  539  GGTCCCTGGAGGGAGGCAGAGAGAGAGAGAGAAAAAAAAAAAAAACCCAGCTCCTGGAAC  598

Query   778  AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTG-CCTCCGTTTCTCCCCAG  836
          |||||
Sbjct  599  AGGGAGAGCGCTGGCCTCTTGCTCTCCAGCTCCCTCTGTTGCCCTCCGTTTCTCCCCAG  658

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Query	837	GCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGTCCTGGCTTCAAGAGG	896
Sbjct	659	GCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGCCCTGGCTTCAAGAGG	718
Query	897	GCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAACGCTATGCTCCGCGCCC	956
Sbjct	719	GCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGTACAATGCTATGCTCCGCGCCC	778
Query	957	GTCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTAATGG	1016
Sbjct	779	ATCGCCTGTACCAGCTGGCATATGACACCTATCAGGAGTTTGTAAGCTCTTGGGTAATGG	838
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	839	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGACTTTCCCCCGCTGGGAAGTAATGGGAGGAG	898
Query	1077	ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACTGAG	1136
Sbjct	899	ACTAAGGAGCTCAGGGTTGTTTTCTGAAGTGAAAATGCAGGCAGATGAGCACACGCTGAG	958
Query	1137	TGAGGTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGGCGGT	1196
Sbjct	959	TGAGGTTCCCAGAAGAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGGCGGT	1018
Query	1197	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAACC	1256
Sbjct	1019	CCTTCTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATTCATTCTGCAGAACC	1078
Query	1257	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	1316
Sbjct	1079	CCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCCAACACCTTCCAACAGGGTGAAAACGC	1138
Query	1317	AGCAGAAATCTGTGAGTGGATGCCTTCTCCCCAGGTGGG-ATGGGGTAGACCTGTGGTCA	1375
Sbjct	1139	AGCAGAAATCCGTGAGTGGATGCCTTCTCCCCAGGTGGGGATGGGGGAGACCTGTGGTCA	1198
Query	1376	GAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAACCTAGAGCTGCTCCG	1435
Sbjct	1199	GAGCCCCCGGGCAGCACAGCCACTGCCGGTCCTTCCCCTGCAGAACCTAGAGCTGCTCCG	1258
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	1495
Sbjct	1259	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTT	1318
Query	1496	CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTGAAGGACCT	1555
Sbjct	1319	CGCCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATCGCCACCTAAAGGACCT	1378
Query	1556	AGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC--AATCCTGG	1612
Sbjct	1379	AGAGGAAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGGATCCCCAATCCTGG	1438
Query	1613	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	1672
Sbjct	1439	GGCCCCACTGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTCTTTTAGCAGTCA	1498
Query	1673	GGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCT	1732
Sbjct	1499	GGCGCTGACCCAAGAGAACTCACCGTATTCTTCATTTCCCCTCGTGAATCCTCCAGGCCT	1558

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Query 1733 TTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTG 1792
          |||
Sbjct 1559 TTCTCTACAACCTGGAGGGGAGGGAGGAAAATGGATGAATGAGAGAGGGAGGGAACAGTC 1618

Query 1793 CCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAAGATGGCAGCC 1852
          |||
Sbjct 1619 CCCAAGCGCTTGGCCTCTCCTTCTCTTCTTCACTTTGCAGAGGCTGGAGGATGGCAGCC 1678

Query 1853 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 1912
          |||
Sbjct 1679 CCCGGACTGGGCAGATCTTCAATCAGTCCTACAGCAAGTTTGACACAAAATCGCACAAACG 1738

Query 1913 ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG 1972
          |||
Sbjct 1739 ATGACGCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAGG 1798

Query 1973 TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 2032
          |||
Sbjct 1799 TCGAGACATTCTGCGCATCGTGCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAGC 1858

Query 2033 TGCCCGGGTGGCATCCCTGTGA 2054
          |||
Sbjct 1859 TGCCCGGGTGGCGTCC-TGTGA 1879

```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Mar 1, 2009 5:49 PM

Number of letters in database: 660,889,664

Number of sequences in database: 8,293,739

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Lambda      K      H
      1.33    0.621    1.12
Gapped
Lambda      K      H
      1.28    0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 8293739
Number of Hits to DB: 7398931
Number of extensions: 2386
Number of successful extensions: 2386
Number of sequences better than 10: 1140
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 2296
Number of HSP's successfully gapped: 2295
Length of query: 2660
Length of database: 26430693440
Length adjustment: 34
Effective length of query: 2626
Effective length of database: 26148706314
Effective search space: 68666502780564
Effective search space used: 68666502780564
A: 0
X1: 15 (28.8 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 15 (28.8 bits)

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S2: 23 (43.6 bits)